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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model Run on: March 28, 2003, 09:01:30 ; search time 68.7874 Seconds (without alignments) 251.615 Million cell updates/sec. Sequence: 1 0686CSSQSISPMRSISENSPTASSQSSATNMAIHRSOP 84	Searched: 671580 seqs, 206047115 residues Total number of hits satisfying chosen parameters: 74486 Minimum DB seq length: 40 Maximum DB seq length: 90	Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 1000 summaries Sammaries Sammaries 1. **Spinate *** 2. **Sp. bacteria:** 4. ***Sp. linearie** 5. **Sp. linearie** 6. **Sp. mammal:** 7. **Sp. linearie** 8. ***Sp. linearie** 10. ***Sp. linearie** 11. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 10. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 10. ***Sp. linearie** 11. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. **Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 10. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 19. ***Sp. linearie** 19. ***Sp. linearie** 11. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 19. ***Sp. linearie** 19. ***Sp. linearie** 11. ***Sp. linearie** 12. ***Sp. linearie** 13. ***Sp. linearie** 14. ***Sp. linearie** 15. ***Sp. linearie** 16. ***Sp. linearie** 17. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 18. ***Sp. linearie** 1	licted by chanc e of the resul score distrib	62.5 14.8 67 16 58 13.7 8 67 16 54 13.2 58 9 54 12.8 80 5 51 12.5 80 12 51 12.5 80 12 48.5 11.5 66 5 48.5 11.5 66 15 47.5 11.2 90 12 47.5 11.2 90 16 47 11.1 86 15 47.5 11.2 90 16 47 11.1 86 15 47 11.1 86 15

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086983 mycobacteri
                                                                                                                                                                                   immun
O9ycbl aeropyrum p
O9wphO wild ass he
O9z383 escherichia
                                                       O9juz7 neisseria m
O99j81 rattus norv
O8yhd0 brucella me
                                                                                                                         Q8uj23 agrobacteri
Q9x8d9 streptomyce
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022336 stellaria 1
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Kinashi H., Hopwood D.A.;
A set of ordered cosmids and a detailed genetic and physical map for the 8 km Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                            human
                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL_TaxID-1902;
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
                                                                                                                                                                                                                                                                                               67 AA
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Q9MZQ6
Q9M638
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Q99Y06
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MEDLINE-97000351; PubMed-8843436;
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01-JUN-2002 (TEMBLrel. 21, Le
Hypothetical protein SC03984.
SC03984 OR SCBAC25E3.21.
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  STRAIN-A3(2);
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STRAIN-A3(2) / W145;

STRAIN-A3(2) / W145;

Benelley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Ollver K., O'Nell S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warfen T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces
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NCBL_TaxID=29252;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 67 AA; 7054 MW; F55E8A16E8005067 CRC64;
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Pred. No. 7.4;
6; Mismatches 15;
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Nature 417:141-147(2002).
EMBL, AL596251; CAC44708.1;
InterPro: IPR001281; Rieske.
PROSITE; PS00200; RIESKE_2; UNKNOWN_1.
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01-MAR-2002 (TrEMBLrel. 20, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Hypothetical 7.9 kDa protein.
Homo sapiens (Human).
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Local Similarity 40.5%;
Hes 15; Conservative
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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SEQUENCE FROM N.A.

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YbgA protein.
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                Xue 0.;
"Studies on the tail region of the temperate coliphage 186 genome.";
Thesis (1993), University of Adelaide.
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                                                        MEDLINE-88371265; PubMed-9705261;
MEDLINE-88371265; PubMed-9705261;
Portelli R., Dodd I.B., Xue O., Egan J.B.;
The late-expressed region of the temperate coliphage 186 genome.";
Virology 248:117-130(1998).
EMBL: U32222; AAC34169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                 13.2%; Score 56; DB 9; Length 58; 38.5%; Pred. No. 35; tive 6; Mismatches 10; Indels
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"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"My 140802; AaKi 19010.1;
"Hypothetical protein.
SEQUENCE 80 AA; 8481 MW; AE43A8268EEB6C423 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of C. elegans cosmid 2C477.";
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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51 51 Q -> *.
58 AA; 6491 MW; 1199113D8CDEB8E6 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 8.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                        80 AA.
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MEDLINE-99069613; Pubmed-9851916;
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23; Conservative
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Shimizu H., Saitoh Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.; "Complete nucleotide sequence of the F plasmid: Its implications for organization and diversification of plasmid genomes."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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"Twelve 43-base-pair repeats map in a cis-acting region essential for partition of plasmid mini-F.";
J. Bacteriol. 165:1043-1045(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-90317835; PubMed-2164585; Yoshioka Y., Fujita Y., Ohtsubo E.; "Nucleotide sequence of the promoter-distal region of the tra operon of plasmid R100, including traI (DNA helicase I) and traD genes."; ") Mol. Biol. 214:39-53(1990).
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BEDLINES #8194554.
Saadi S., Maas W.K., Hill D.F., Bergquist P.L.;
Mass W.K., Hill D.F., Bergquist P.L.;
Notlochide sequence analysis of RepFIC, a basic replicon present in IncFI plasmids P307 and F, and its relation to the RepA replicon of IncFI plasmids.";
J. Bacteriol. 169:1836-1846(1987).
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                                                                                                                                                                                                                                                                           Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95337425; PubMed=7612932;
Broom J.E., Hill D.F., Hughes G., Jones W.A., McNaughton J.C.,
Stockwell P.A., Petersen G.B.;
"Sequence of a transposon identified as Tnl000 (gamma delta).";
DNA Seq. 5:185-189(1995).
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F Plasmid DNA complete mini-F region (F coordinates 40.301F to
49.869F).".
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                                                                                           Last sequence update)
Last annotation update)
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   84 AA.
                                           01-007-2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last seq)
01-00T-2000 (TrEMBLrel. 15, Last anno
PRT;
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MEDLINE-86139869; PubMed-3949712;
PRELIMINARY;
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PRT;
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SMART; SM00247; XTALbg; 1.
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les 17; Conservative
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NCBI_TaxID=8355;
                                 Best Local Similarity
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64 RVGS 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21844071; Pubmed-11853398;
Chen L.L., Leu J.H., Huang C.J., Chou C.M., Chen S.M., Wang C.H.,
Lo C.F., Kou G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21342572; PubMed=11448154; van Hulten M.C.W., Witteveldt J., Peters S., Kloosterboer N., Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.; "The white spot syndrome virus DNA genome sequence."; Virology 286:7-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. witteveldt J., Peters S., Kloosterboer N., Tarchini R., Fiers M., Sandbrink H., Lankhorst R.K., Vlak J.M.; Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.; Complete genome sequence of the shrimp white spot bacilliform
12.8%; Score 54; DB 16; Length 84; 38.2%; Pred. No. 94; tive 2; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOC.F., Kou G.-H.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AF360029; AAR77731.1; -.

EMBL, AF332093; AAL3901.1; -.

EMBL, AF440570; AAL89012.1; -.

SEQUENCE 80 AA; 8806 MW; 92462B3C00342FB1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Yang F., Pan D., Zhang X., Xu X.; Yang F., He J., Lin X., Li Q., Pan D., Zhang X., Xu X.; Submitteed (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
0RF62 (Wsv087) (WSSV144).
White spot syndrome virus (WSSV).
Viruses; unclassified viruses.
                                                                                                                                     43 AMRAGGCIHPSGRWCPVASSTVPATGLHQHHSDP 76
                                                                                                   51 AWRKKGCLRLGTHGSPTASSQSSATNMAIHRSQP 84
                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-21548311; Pubmed-11689662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virol. 75:11811-11820(2001).
                        Local Similarity 38.2 es 13; Conservative
                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-92652;
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           Query Match
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cches 23; Indels 14; Gaps
                                                                                                           13 PMRSISENSLVAMDFSGQKSRV-----IENPTEALSVAVEEGLAWRKKGCLRLGTHG 64
                                                                                                                                                      6 PVARSGPHSVGELAFDGKFLEVGVRGDNLYISEPGQARSISLSRGTA------KHT 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 RSGCSSQSISPMRSISENSLVAM----DFSGQKSRVIENPTEALSVAVEEGLAWRKKGCL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPGNENTS OF THE VERTEBRATE EYE LENS (BY SIMILARITY).
-! DOMIN: HAS A TWO-DOMIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS (BY SIMILARITY).
-! SIMILARITY: BELONGS TO THE BETA-GAMMA-CRYSTALLIN FAMILY.
EMBL, RE035565; AAB87702.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Beta Bl-crystallin (Fragment).
Xenopus laevis (African clawed frog).
Eukaryota: Metachia: Chordata: Craniata: Vertebrata: Euteleostomi;
Amphibia: Batrachia: Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CG18844 protein.
CG18844 prosphila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 13; Length 88;
Pred. No. 2.2e+02;
12.5%; Score 53; DB 12; Length 80; 25.6%; Pred. No. 1.2e+02; Live 12; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-97312614; PubMed-9169055;
Altmann C.R., Clow R.L., Lang R.A., Hemmati-Brivanlou A.;
Lens induction by Pax-6 in Xenopus laevis.";
Dev. Biol. 185:119-123(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 88
88 AA; 10461 MW; A9164E3275EE0E1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1 Duplication; Eye lens protein.
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RA Addmas M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addmas M.D. Celnikers S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Gorge R.A., Lewis S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Mannatides P.G., Scherer S.E., in P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Hortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M. Basu A. Bascendale J., Bayraktaroglu L., Beasley E.B.,
RA Ballew R.M. Basu A. Baxendale J., Bayraktaroglu L., Beasley E.B.,
RA Berkova D., Botchan M.R., Bouck J. Brokstein P., Brottler P.,
RA Burris K.C., Busmen D.A., Dallle C., Davenbort L.B., Cheer A., Chandra I.,
RA Burris K.C., Busm D.A., Dallle C., Davenbort L.B., Davies P.
RA Burris K.C., Busm D.A., Dallle C., Perraz C., Certera P., Erottler P.,
RA Bollos B., Delicher A., Deng J. Mays A.D., Dew I., Dietz S.M.,
RA Bollos B., Delicher A., Deng S., Mayshakov S., Pleischmann M. Posler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Bosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Bouck J., Harvey D., Helman T.J., Hernandez J.R., Bouck J., Mosheri M. A., Jalali M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Retchum K.A., Hannel B.E., Kodire C.D., Worris S., Kaup D. D., Lai Z., Kanson D.L.,
RA Mannel B.E., Kodire C.D., Warris M. Harris N.L., Mattet B., McIntoon T.C., Morris J. Wosherfi N. Moy M., Wurphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Blazzolo M., Pittnan G.S., Pen S., Pollard J., Worles M., Shipski M.P., Smith T.,
RA Shient R., Nelson K.A., Nixon K., Worls, M., Wolssenbech J., Was Sprach M., Wolssenber S., Wolssenbech J., Was Sprach M., Wolssenber S., Wolssenbech J., Was Sprach M., Wolssenber S., Wolssenber J., Was Spra
    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
NCBI_TaxID=7227;
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Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
NGBL_TAXID-9612;
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PROSITE; PS00063; ALDOKETO_REDUCTASE_3; UNKNOWN_1.
SEQUENCE 65 AA; 7223 MM; 5EE4BC8FEDC92DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II antigen beta chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 RSGCS-----SQSISPMR-SISENSLVAMDFSGQKSR 33
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                                                                                    SEQUENCE FROM N.A.
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[1]
SEQUENCE FROM N.A.
Kennedy L.J., Angles J.M.;
Nomenclature for the DLA system, 2000: Second report of the ISAG DLA
Nomenclature Committee.",
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF343738; AAK13709.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-A tumefaciens; STRAIN-MAFF301001; PLASMID-PTI-SAKURA; MEDLINE-9913120; PUMBG4=954202; Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.; "Novel structural difference between nopaline: and octopine- type gene:construction of genetic and physical map and sequencing of Lib/trai and rep gene clusters of a new Ti plasmid PTi-Sakura."; Biochim. Biophys. Acta 1396:1-7(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-A tumefaciens; STRAIN-MAFF301001; PLASMID-PTI-SAKURA; MEDLINE-D018475; PubMed-10721727; Suzuki K., Battori Y., Uraji M., Ohta N., Iwata K., Murata K., Catch A., Yoshida K.; Complete nuclectide sequence of a plant tumor-inducing Ti plasmid."; Gene 242:331-336(2000).
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                            2 GRSGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLG 61
                                                                                                                                                                                                                                                                                        16 GRSGCGSWRDTSITGRSTCASTATWGSTGRSRSGGPT--LSPGTRRRSSWSGR-----G 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA(I): Strategy for DNA sequencing of Japanese cherry-ri plasmid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Obta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.; "Genome structure of pTi-SAKURA (III): Characteristics of T-DNA."; Nucleic Acids Symp. Ser. 39:185-186(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobacterium tumefaciens, and
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Plasmid pTi-SAKURA, and Plasmid pTiC58.
Bacteria: Proteobacteria: alpha subdivision; Rhizobiaceae group;
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Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
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                                                                                                                                                                                                Score 48.5; DB 7; Length 90;
Pred. No. 4.4e+02;
8; Mismatches 34; Indels
                                                                                                                                        NON_TER 90 90
SEQUENCE 90 AA; 9600 MW; D4F5E19F28AD13AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) TIORF132 protein (Hypothetical protein Atu6153).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 AA.
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01-MAY-2000 (TrEMBLrel, 13, Last sed
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                                                                                                                                                                                              11.5%;
29.0%;
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NCBI_TaxID=358, 176299;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                62 THGSPTASS 70
                                                                                                                                                                                                                                                                                                                                                                69 PRWTPTADT 77
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Best Local Simi
Matches 20;
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EMBL; AF378539; AAK56383.1; -
Hypothetical protein.
SEQUENCE 90 AA; 9906 MW; 28
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                     79 TKGT 82
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                                                                     Query Match
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092209;
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SPECIES-A. tunefaciens (strain C58 / ATCC 33970); PLASMID-PTIC58;
MEDILINE-21608551; PubMed-11741194;
MEDILINE-21608551; PubMed-11741194;
MEDILINE-21608551; PubMed-11741194;
MOUTOLD B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Moulam C., Cardon J., Voudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Moulam C., Allinger M., Doughty D., Scott C., Strub G., Cience Squence of the plant pathogen and biotechnology agent Agrobacterium tunefaciens C58 ";
Refenome sequence of the plant pathogen and biotechnology agent Science 294:233-2328(2001).
REMBL; ABO00434; AAL46389-1; -
REMBL; ABO00434; AAL46389-1; -
REMBL; ABO00434; AAL46389-1; -
REMBL; ABO007941; AAR401116.1; -
REMBL; ABO007941; PLASMID Complete proteome.
WHYPOCHELCAI protein; Plasmid; Complete Proteome.
"Genome Structure of pTi-SAKURA (IV): Characteristics of tra region.";
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MEDLINE-1556188; PubMed-11679351;
Stokes H.W.; Hollmes A.J., Nield B.S., Holley M.P., Nevalainen K.M.H.,
Mabbutt B.C., Gillings M.R.; Gene Cassette PCR: Sequence-Independent Recovery of Entire Genes from
Environmental DNA.,
Appl. Environ. Microbiol. 67:5240-5246(2001).
                                                                                                                                                               SPECIES—A tumefactens (strain C58 / ATCC 33970); PLASMID—PTIC58; WEBLINES-12068550; PubMed-11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.P. JT., Woo L., Chen Y., Paulsen IT., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Chumley F., Tingey S.V., Tomb J.F., Gordon M.P., Olson M.V.,
                                                                                                                                                                                                                                                                                                                                                 genome of the natural genetic engineer Agrobacterium tumefaciens
                                                             SPECIES-A.tumefaciens; STRAIN-MAFF301001; PLASMID-PTI-SAKURA; Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.; "Genome structure of PTI-SAKURA (Y): Complete nucleotide sequence of plasmid PTI-SAKURA (Y vir region in Agrobacterium tumefaciens."; Nucleic Acids Symp. Ser. 39:265-266(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 16; Length 89;
Pred. No. 5e+02;
5: Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypotherical 9.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 SGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 SQRKSRV-----PCSLAVISSMLHRQKGAVRLG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; environmental samples. NCBI_TaxID=2338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch
l Similarity 41.2%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  Science 294:2317-2323(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                               SEQUENCE FROM N.A
                                                                                                                                                    SEQUENCE FROM N.A
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M
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                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkontlo H., Leinitki P., Salminen M.O.;
Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
HSSP, P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
NCBL_TaxID-382;
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MEDLINE-21396509; PubMed-11481432;
MEDTINE-21396509; PubMed-11481432;
MEDTINE-A.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barlot-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 47.5; DB 15; Length 66; ilarity 35.9%; Pred. No. 4e+02; Conservative 4; Mismatches 20; Indele 1
                                                                          11.3%; Score 48; DB 2; Length 90; 28.1%; Pred. No. 5.1e+02; Live 14; Mismatches 26; Indels
al protein.
90 AA; 9906 MW; 281676BA0DAEA28A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 66 66
SEQUENCE 66 AA; 7236 MW; F74E42EF9F24AD6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Greated)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
4e+02;
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 DFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 NFKGOR-RXLSASTVAEGHLARNCRAPRKKGCWKCGKEG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein RA0390.
RA0390 OR SMA0736.
Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 AA.
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gag protein (Fragment).
                                                                                                     Local Similarity
es 18; Conserv
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SEQUENCE FROM N.A. STAINSPOSON-TYSO44; MEDIAINE-994049312; Pubbled-10476039; MIDAKHINA S., Kholodii G., Mindlin S., Yurieva O., Nikiforov V.; Minakhina S., Kholodii G., Mindlin S., Yurieva O., Nikiforov V.; Sirsosofora are res site hunters sensing plasmidal res sites occupied by cognate resolvases."; Microbiol. 33:1059-1068(1999).
                                                                                                                                                                                                                                                                         4 RSGPTSHPVRPTLGVAELA-VQMNHPGAGGDC--DLTRRMQIWVHQGSSMLRRGSGQMAW 60
                                                                                                                                                                                                                                      3 RSGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLG- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GRSGCSSQSISPMRSISENSLVA--MDFSGQKSRVIE-NPTEA-LSVAVEEGLAWRKK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2] SEQUENCE FROM N.A. SPECUENCE FROM N.A. STRAIN-TAP44-3; TRANSPOSON-TNS044; Kholodii G., Yurieva O., Mindlin S., Gorlenko Z., Rybochkin V., Nikiforov V.; """ famenacon coding for temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Tn5044, a novel Tn3 family transposon coding for temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 46.5; DB 2; Length 79; 31.0%; Pred. No. 6.5e+02; ive 14; Mismatches 15; Indels 1
                                                                                                                                                                             Length 86;
                                                                                                                                                                    11.1%; Score 47; DB 2; Length 86; 22.0%; Pred. No. 6.38+02; tive 18; Mismatches 40; Indels
                                                                                                                                   86 AA; 9140 MW; CB240A7B86386B18 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 8:6 KDa protein.
Xanthomonas campestris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable ribosomal protein S19, mitochondrial.
B1109.070.
                                                                                                                                                                                                                                                                                                                                                                                                                                              79 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sensitive mercury resistance.";
Res. Microbiol. 151:1-12(2000).
EMBL, Y17691, CAB65713.1;
Hypothetical protein; Plasmid.
SEQUENCE 79 AA; 8626 MW; 16:
                                                                                                                                                                                                                                                                                                              62 -- THGSPTASSQSSATNMAIHR 81
                                                                                                                                                                                                                                                                                                                                               61 RVAHVHPTLAEGVNTAAGGVHR 82
                                                                                                                                                                                   Local Similarity 22.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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es 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurospora crassa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmid pKLH443
                                                                                                                                                                      Query Match
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Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H., Per K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire Sinorhizobium mellioti psymh megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL; ABO07230; ARK65048.1;
Hypothetical protein; Plasmid; Complete proteome.
SEQUENCE 90 AA; 9914 MW; CC9E8095982DDID5 CRC64;
                                                                                                                                                                                                                19; Gaps
                                                                                                                                                                                                                                      11 ISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAW-----RKKGCLRL-GT 62
                                                                                                                                                                                                                                                               Ol-JAN-1998 (TrEMBLrel. 05, Created)
Ol-JAN-1998 (TrEMBLrel. 05, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last amontation update)
Plasmid pFAJZ600 putative plasmid multimer resolution protein (pmrA),
putative DNA-binding replication protein (repB), putative replication
Protein (repA), and putative plasmid partitioning protein (parA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi;
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus.
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Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
                                                                                                                                                                    11.2%; Score 47.5; DB 16; Length 90; 22.1%; Pred. No. 5.8e+02; tive 15; Mismatches 19; Indels 19
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MEDILMS-98015402; PubMed-9353918;
De Mot R., Nagy I., De Schrijver A., Pattanapipitpaisal P., Schoofs G., Vanderleyden J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 11; Length 79; Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026208; AAH26208.1; -.
SEQUENCE 79 AA; 8632 MW; 806C30C3455C10BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                79 AA.
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01-JUN-2002 (TrEMBLrel. 21, Last segments)
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                   Local Similarity 22.19
es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
es 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodococcus erythropolis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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TISSUE-THYMUS GLAND;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similar to LOC164714
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                                                                                                                                                                                                                                                                                                              63 HGSPTASS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                             60 RKTNTPSS 67
                                                                                                                                                                      Query Match
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030681
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Cysteine proteinase (Fragment).
Marcissus seudonarcissus (Daffodil).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Amaryllidaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AA.
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01-WAR-2002 (TrEMBLrel. 20, Last sequence
01-WAR-2002 (TrEMBLrel. 20, Last annotative
Putative MYB family transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=39639;
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                                                                                                                                              Narcissus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Q76048
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MEDLINE-21082930; PubMed-11214968;
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MEDLINE-21082930; PubMed-11214968;
MEDLINE-21082930; PubMed-11214968;
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                                                                                                                        SEQUENCE FROM N.A.
Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
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EUkaryOta; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBL_TaxID-5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.0%; Score 46.5; DB 3; Length 80; 25.0%; Pred. No. 6.6e+02; tive 14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 MRSISENSLVAMDFSGQKSRV-IENPTEALSVAVEEGLAWRKKGCLRLGT 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 MSILSSLGRIATEFSAARARYQTERAIRSLPIELQKDIGWPEASDTKTGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.0%; Score 46.5; DB 16; Length 822.0%; Pred. No. 7.48+02; Live 13; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |:|:|: : : : : | | | : | | : | | : | | 30 KKIAPIRTQARSATILPNFVGLKFQV-HNGKDYIDLIVTEEMVGHKLG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 QSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKG 56
                                                                                                                                                                                                                                                                                                               German Neurospora genome project;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AL513409; CAD11378.1;
InterPro; IPR002222; Ribosomal_S19.
Probom; PP0010012; Ribosomal_S19; 1.
Ribosomal protein.
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NDNA Res. 7:331-338 (2000).

EMBL; APO02997; BAB48667.1; -

Hypothetical protein; Complete proteome.

SEQUENCE 88 AA; 9552 MW; DA4EE5FE549D2D2C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 AA; 9018 MW; DA38F8D77C20E041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2001 (TIEMBLrel. 18, Created)
01-OCT-2001 (TIEMBLrel. 18, Last sequence update)
01-OCT-2001 (TIEMBLRel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 25.0% es 12; Conservative
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Q93WW8
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AC Q93WW6
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STRAIN-CV. DUTCH MASTER; TISSUE-SENESCING TEPALS OF 4-DAY OLD FLOWERS; Hunter D.A., Yi M., Reid M.S.; Roole of Ethylene and ABA in Detrainth Senescence of Daffodil (Narcissus pseudonarcissus L. Dutch Master)."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR0018, AALL6903.1; ABBL/GenBank/DDBJ databases. InterPro; IPR002086; Aldehyde.dehydr.
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Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C., L., Bowser L., Jones T., Banh J., Carrinci P., Chen H.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Saton M., Seki M., Shinn P., Yamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AY072387; AAL62379.1;

SEQUENCE 54 AA: 6078 MW; ZA9E672F34B7BEDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Makaryota, Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudiootyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 11.0%; Score 46.5; DB 10; Length 90; Best Local Similarity 33.3%; Pred. No. 7.6e+02; Matches 24; Conservative 13; Mismatches 22; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 QGR--CSSKK-SPIVSIDGYQNVPVNNEAALMKAVAN--QPVSVAIEASGMAFQFYSEGV 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QGRSGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVE-EGLAWR--KKGC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.9%; Score 46; DB 10; Length 54; 31.7%; Pred. No. 4.6e+02; Live 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 90 90
SEQUENCE 90 AA; 9546 MW; 5B7C407359B3A658 CRC64;
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ProDom; PD000158; Peptidase_C1; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
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                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 MRSISENSLVAMDF----SGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSP 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.9%; Score 46; DB 16; Length 87;
                     38.1%; Pred. No. 8.2e+02;
tive 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 8.3e+02;
tches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRT-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xfa00004.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                 87 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 AA.
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les 16; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20365717; PubMed-10910347;
                                                                                                                                       47 EEGLAWRKKGCLRLGTHGSPT 67
                                                                                                                                                                                                                 39 EDGLVYEGRGWNTVGAHSGPT 59
                          Best Local Similarity 38.13
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa.
Plasmid pXF51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=2371;
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                                                                                                                                                                                                                                                                                                                                  RESULT 23
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                                                                                                                                                                                                            QΩ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 15; Length 77;
Pred. No. 7.2e+02;
7; Mismatches 14; Indels 28; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Salminen M.O.; "Rapid and simple characterization of in vivo HIV-1 sequences using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rapid and simple characterization of in vivo HIV-1 sequences using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kappeler S.R.; "The peptidodytycan recognition protein, PGRP, is expressed in the lactating mammary gland of camels."; submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ310355; CAC83647.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEPTIDOGLYCAN RECOGNITION PROTEIN.
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SEQUENCE 77 AA; 8724 MW; 2BEAEEB9B5C5E6A6 CRC64;
                                                                 01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01.WAR-2002 (TrEMBLrel. 20, Last annotation update)
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9517 MW; BFC5DC02AF11CBE5 CRC64;
                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pepridoglycan recognition protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  solid phase direct sequencing.";
AIDS Res. Hum. Retroviruses 0:0-0(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR01878; Znf_CCHC.
Pfam; PF000089; zf-CCHC; 2.
PRINTS; PR00939; CZHCZARFINGER.
SMART; SM00343; Znf_CZHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.9%;
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es 15; Conservative
PRELIMINARY;
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                                                                                                                                                                                               P24/P25/P7 (Fragment).
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TISSUE-ADIPOSE TISSUE;
                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-11676;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GKEG 64
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SEQUENCE
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08WMP:
AC OBWMP:
AC OBWMP:
DT 01-MAI
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Matches
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WEDLINE—20365717; Pubbwed=10910347;

X MEDLINE—20365717; Pubbwed=10910347;

A Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,

A Alvarenga R., A., Reinach F.C., Arruda P., Bare G.S., Baptista C.S.,

B Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.W., Briones M.R.S.,

B Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.W., Briones M.R.S.,

B Barros M.H., Colombo C., Costa F.F., Costa M.C.R., Carrer H.,

A Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.N.,

R Coluthho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,

Facilican A.P., Ferreira A.J.S., Ferrero J.A.,

R Facilican M. Colomen G.H., Goldman M.H.S., Gomes S.L., Kitajian J.P.,

A Krieger J.E., Kuramae E.E., Laigret F., Lambals M.R., Leite L.C.C.,

A Marchaed M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,

A Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,

Mon D.H., Nayai M.A., Nascimento A.L.T.O., Netto L.E.S.,

R Mon D.H., Nobrega F.G., Nunes L.R., Olivetra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashi T., Kamio Y., Hishinuma F., Usami Y., Titani K., Terawaki Y.;
"Pseudomonas aeruginosa cytotoxin; the nucleotide sequence of the gene and the mechanism of activation of the protoxin.";
Mol. Microbiol. 3:861-868(1989).
EMBL; AB0008550; BAA36239.1;
SEQUENCE 89 AA; 9239 WW; B3A0DIC2798852E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=PHICTX-C;

MEDLINE-29157549; PubMed=10027959;

Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;

Nakayama K., Kanaya S., Ohnishi M., Terawaki Y., Hayashi T.;

"The complete nucleocitde sequence of phicTx, a cytotoxin-converting phage of Pseudomonas aeruginosa: implications for phage evoltion and horizontal gene taransfer via bacteriophage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                          Viruses; data viruses; no RNA stage; Caudovirales; Myoviridae.
NCBL_TAXID-153AA viruses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE-GLAW 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 89;
                                                                                                                                                                                                                                                                           Hayashi T.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf1634.
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30.0%; Pred. No. 8.5e+02;
tive 10; Mismatches 23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [3]
SEQUENCE FROM N.A.
STRAIN-PHICTX-C;
MEDLINE-90014160; Pubmed-2507866;
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                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-PHICTX-C;
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Local S.
15;
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09PCX0
DD Q9PCX
DJ Q
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RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoco B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA de Groad V.E. Jr., de Sa R.G., Sandelli R.V., de Rosa A.J.M.,
RA da Silva A.C.R., da Silva P.R., Silva M.A. Jr.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA da Silva M.A., Verjovski-lmeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meddanis J., Setubal J.C.,
RT Ynde ganome sequence of the plant pathogen Xylella fastidiosa.";
RT Who ganome sequence of the plant pathogen Xylella fastidiosa.";
RT Nature 406:151-159(2000).
BRE. ABO3990; AAF84443.1; -.
BRE.
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P29827 Streptovert P52870 saccharomyc P75576 mycoplasma P101132 mycoplasma P01012 mycoplasma P01019 homo sapien P05560 dromaius no 038666 bacteriopha P22755 bacillus 11 P00202 methanosarc P10624 desulfovibr P7613 escherichia P58091 caulobacter P47401 mycoplasma O61616 mus musculu 099pqq6 ureaplasma P07441 lathyrus ap P05559 casuarius c P01418 dendroaspis Q01418 dendroaspis Q0139 mus musculu Q0502 escherichia P50483 methanobact O70139 mus musculu Q0502 escherichia P12732 haloarcula P14073 butyribacte O28560 archaeoglob P04417 dendroaspien O1881 macaca radi Q922b9 homo sapien O1881 macaca radi Q922b9 homo sapien P15732 haloarcula P14073 butyribacte O28560 archaeoglob P04417 dendroaspien O1881 macaca radi Q9205 centruroide P32005 papio hamad P01495 centruroide	P55597 rhizobium s 030153 archaeoglob 088514 rattus norv P50115 bos taarus 039511 casuarina g P16001 paramecium 09494 arabidopsis 007112 mastigoclad P5744 saccharcmyc P58190 sulfolobus P56531 meleagris g 09477 aeropyrum p 005551 leishmania 0905651 leishmania 0905651 leishmania 0905651 leishmania 0905651 leishmania 090568 bos taurus P12350 euplotes ra P12350 eutloman mumun P1355 escherichia P1355 eacholepea P1355 escherichia P1355 eacholepea P1355 escherichia P1355 escherichia P1355 eacholepea P1355 escherichia P1355 escherichia P1355 escherichia P1355 escherichia P1355 escherichia
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model Run on: March 28, 2003, 08:56:00; Search time 18.51 (without alignmen 18.51 (without alignmen 18.51 (without alignmen 18.51 (without alignmen 18.52 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	

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Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
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NCBI_TaxID=10665;
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Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 8.1 kDa protein in ndd-denB intergenic region.
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SEQUENCE FROM N.A.
Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
Kutter E., Arisaka F., Kunisawa T., Thomas E.;
Mesyanzhinov V., Ruger W., Stidham T., Thomas E.;
"Bacteriophage T4 genome analysis.";
"Bacteriophage T4 genome analysis.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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ZINC (BY SIMILARITY).
E716EA406D65B831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 71 AA; 8143 MW; 5D56546D2FADAFOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 ISPLKSTSEKMTVNATLANNSNERFCIENDTETYTV 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 AA.
                                                                                                                                                                                                                                                                                                                                               71 AA.
                                                                                                                                           ch 12.2%; Score 51.5; D
1 Similarity 30.0%; Pred. No. 29;
15; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                 PRT;
                    Metal-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF158101; AAD42616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MJECL05. MJECL05.
                                                                                         45 45
73 AA; 8695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                             STANDARD;
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es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical 8
Y16K OR NDD.1.
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Q60262;
                                                                                                                                                                                                                                                                                                                                                 Y16K_BPT4
                                                                                                            SEQUENCE
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Matches
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informatics and the EMBL outstation -
e. There are no restrictions on its
long as its content is in no way
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                                                        helicobacte
rhizobium s
                                                                                             bos taurus
aptostichus
                                                                                                                                 escherichia
serratia ma
                                                                                                                                                                                                                                                          mus musculu
                                                                                                                                                                                                                                                                          xenopus lae
                                                                                                                                                                                                                                                                                           helianthus
escherichía
                      bacteriopha
                                       maguari vir
                                                                                                                                                                                                        azospirillu
                                                                                                                                                                                                                        bacteriopha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou L., Fleischmann R.D., Gozayne J.D., Pald L.W., Clayton R.A., Gocayne J.D., Stoch K.G., Merrick J.M., Glodek A., Idman J.F., Pihrmann J.L., Mouyen D., Grson J.D., Sadow P.W., Hanna M.C., M.A., Kaine B.P., Borodovsky M., H.O., Weese C.R., Venter J.C.s. methanogenic archeeon, Methanococcus
                                                                                                                                                                                                                                         morganella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAEBACTERIA RPON / EUKARYOTIC RPB10
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79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metallothionein-like protein type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequ
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Z11663; CAA77731.1; -. EMBL; U49062; AAA91470.1; -.
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56
76
27
37
48
56
7862 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002
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024058;
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CARBOHYD
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                     STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

BULT C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Overbeek R.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Scott J.L., Geoghagen NS.M., Weldman J.F., Fuhrmann J.L., Nguyen D.,
Cutterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Magnaldo T.A., Barrandon Y.;

7024 (hear stable antigen, nectedrin), a novel keratinocyte
differentiation marker, is preferentially expressed in areas of the
differentiation marker, is preferentially expressed in areas of the
differentiation marker, is preferentially expressed in areas of the
differentiation marker, is preferentially expressed in areas of the
J. Cellicle containing the colony-forming cells.";
J. Cell Sci. 109:3035-3045(1996).

FRIGGERING MEGHANISM OF SIGNAL TRANSDUCTION MAY BE DUE TO THE
INTERACTIONS OF DIFFERENTIATING CELLG WITH THE MATRIX SUBSTRATE
VIA THE CARBOHYDRATE STRUCTURE OF THE MOLECULE. IN THIS WAY, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-MISTAT: TISSUE-Embryonic brain;
MEDLINE-4122434; PubMed-8292828;
Shirasawa T., Akashi T., Sakamoto K., Takahashi H., Maruyama N.,
Hirokawa K.;
"Gene expression of CD24 core peptide molecule in developing brain and developing non-neural tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Signal transducer CD24 precursor (Heat stable antigen) (HSA)
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Indels
                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN 3 15 ILE-RICH.
SEQUENCE 62 AA; 7327 MW; 1624EC72E75EBAD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 RSISENSLVAMDFS-GQKSRVIENPTEALSVAVEEGLAWRKK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 KKVAERFLKDLESSQGMDWKEIRERAERAKKQLEEGIEWAKK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 90;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46.5;
                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Fischer;
MEDLINE-97157759; Pubmed-9004038;
                                                                                                                                                                                                                                                                                                                                                EMBL; L77118; AAC37071.1; -.
                                                                                                                                                                                      Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 28.6 es 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and developing non-neural
Dev. Dyn. 198:1-13(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                  MJECIOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Nectadrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD24_RAT
Q07490;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                  TIGE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL TRANSDUCER CAN PLAY VERY DIFFERENT ROLES IN DIFFERENT CELL TYPES AS A DIRECT CONSEQUENCE OF ITS GLYCOSYLATION.
SUBCELLULAR LOCATION. Attached to the membrane by a GPI-anchor.
TISSUE SPECIFICITY: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM, IN POSTMITOTIC CELLS OF SPINAL CORD, HINDERAIN, MIDBRAIN AND FOREBAIN. EXPRESSED IN POTHILLULAR THE DEVELOPMENT OF NON-MEDICAL TISSUES. EXPRESSED IN POTH DEVELOPMENT, SPECIFICALLY IN PREDAY. AS WELL AS IN THE DEVELOPMENT, SPECIFICALLY IN PRIMATAL BADILLA, AS WELL AS IN THE DEVELOPING EYE AND HAIR FOLLICLE.
DEVELOPMENTAL STAGE: DETECTED IN PRIMITYE ECTODERM, MESODERM AND VENTRAL ENDODERM; DOMN-REGULATED WHEN ORGANGGENESSIE IS COMPLETED.
PIN: EXTENSIVELY O-GLYCOSYLATED (HS SIMILARITY). THE CARBOHYDRATE STRUCTURE MAY BE REGULATED IN A TISSUE SPECIFIC AND DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL TRANSDUCER CD24.

**REMOVED IN MATURE FORM (BY SIMILARITY).

**N-LINKED (GLCNAC...) (POTENTIAL).

**N-LINKED (GLCNAC...) (POTENTIAL).

**PLINKED (GLCNAC...) (POTENTIAL).

**QPI-ANCHOR (POTENTIAL).

42846E70EC39D958 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 CNOTSVAP-----RSGNOSISAAPNPINATT------RSGC----- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 CSSQSISPMRSISENSLVAMDFSGQKS-RVIENPTEALSVAVEEGLAWRKKGCLRLGTHG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; GPI-anchor; Membrane; Signal; Differentiation. SIGNAL 1 26 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
                                                                                                                                                                                                                                                                                                                                    STAGE SPECIFIC MANNER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.6%; Score 45; DB 1; 1 24.4%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-84117462; Pubmed-6320000;
Murphy E., Locadahl S.;
"Transposition of Fin554 does not generate a target duplication.";
Nature 307:292-294(1984).
-i- FUNCTION: INVOLVED IN DAR REPAIR (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE RADC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
9
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last anotation update)
DNA repair protein radC homolog (25 kDa protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 1; Lenger ored, No. 1.86+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SGCSSQSISPMRSISENS---LVAMDFSGQKSRVIENPTEALSVAVEEG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 SGCNGCGMAPDLSYMEGSTTETLVMGVAPQKSHM---EASEMGVAAENG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 82;
Pred. No. 1.9e+02;
7; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAN-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                          InterPro; IFR000347; Metallothlon_15.
Pfam: PF01439; Metallothlon_2; 1.
ProDom; PD001611; Metallothlon_15; 1.
Metal-binding; Metal-thiolate cluster.
SEQUENCE 79 AA; 7836 MW; 8ADC58BID8B644CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 82 AA; 8920 MW; 65E8BF06E3DEC3A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K02985; AAA26680.1; -.
                                                                                                                                                                                                                                                                                                   EMBL; U61973; AAC23697.1; -.
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ilarity 30.6%;
Conservative
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PROSITE: PS01302; RADC: 1.
DNA repair. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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es 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-RN450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RADC_STAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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27 FSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTH--GSPTASSQSSATNMAI 79

ilarity 27.3%; Pre Conservative 7;

Local Similarity es 15; Conserv

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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-20277477; PubMed-10819326; MEDLINE-20277477; PubMed-10819326; Hurowitz E.H., Melnyk J.M., Chen Y.J., Kouros-Mehr H., Simon M.I., Shizuya H.; "Genomic characterization of the human heterotrimeric G protein alpha,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                     Eukaryota; Netazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ή;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein G(!)/G(S)/G(O) gamma-5 like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44.5; DB 1; Length 68;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        869BCA2A081EAA02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
116-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0567.
                                                                                     68 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.7e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43 SVAVEEGLAWRKKGCLRLGTHGSPTASSQSSATN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SVKVSQAAADLKQFCLQNAQH-DPLLTGVSSSTN 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001770; G-gamma.
Pfons, IPR001770; G-gamma.
Promo; Pr00631; G-gamma; 1.
SMART; SM00224; GGL: 1.
PROSITE; PS50058; G-PROTEIN_GAMMA; 1.
PROSITE; PS50058; G-PROTEIN_GAMMA; 1.
                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                    beta, and gamma subunit genes.";
DNA Res. 7:111-120(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF188178; AAF04568.1; -. EMBL; AL031319; CAB41647.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.5%;
38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                     STANDARD;
                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
es 13; Conserv
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057987:
                                                                                     GNGL_HUMAN
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                                                           RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=C trachomatis; STRAIN=D/UW-3/Cx;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
Nucleic Acids Res. 28:1397-1406(2000).
'1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOWAL RNA (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOWAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES—C.muridarum; STRAIN-MOPD / Nigg;
MEDIINE—20150255; PubMed=10684935;
Read T.D., Brunhan R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTH-GSPTAS 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Davis R.W.; "Genome sequence of an obligate intracellular pathogen of humans:
                 -! - SIMILARITY: BELONGS TO THE HMF FAMILY OF ARCHAEAL HISTONES.
                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                  10.0%; Score 42.5; DB 1; Length 67; 25.8%; Pred. No. 2.8e+02; Live 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                              67 AA; 7064 MW; 0AAFCAC535BF2E10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813, 83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             084529; Q9PJLB;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2011 (Rel. 40, Last annotation update)
30S ribosomal protein S19.
RPSS OR RS19 OR CT524 OR TC0811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 AA.
                                                                                                                                                                                                                                             InterPro; IPR003958; CBFA_NFYB_domain.
InterPro; IPR004823; Histone_core.
Pfam; PF00808; CBFD_NFYB_HMF; 1.
DNA-binding; Multigene family.
INII_MET 0 0 0
SEQUENCE 67 AA; 7064 WW; OAAFCAC538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                      , 12;
                                                                                                                                                                                                            EMBL; U12931; AAA67722.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      trachomatis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.";
Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 25.8 es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chlamydia muridarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                         STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
BULL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., Fitzderald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., Tracerald L.M., Clayton R.A., Gocayne J.D.,
Scherbeck R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Darcy T.J., Sandman K.M., Reeve J.N.; "Methanobacterium formicicum, a mesophilic methanogen, contains three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.2%; Score 43; DB 1; Length 82;
25.9%; Pred. No. 3.1e+02;
Live 10; Mismatches 15; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-9138058; pubmed-7836329; Sandman K.M., Grayling R.A., Reeve J.N.; Sandman K.M., Grayling R.A., Reeve J.N.; Unpublished results, Cited by:
Unpublished results, Cited by:
Darcy T.J., Sandman K.M., Reeve J.N.;
J. Bacteriol. 177:858-860(1995).
-!- FUNCTION: BINDS AND COMPACT DNA (95 TO 150 BASE PAIRS) TO FORM NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DNA SUPERCOILS.
-!- SUBUNIT: HOMODIMER OR HETERODIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 SGCSSQSISPMRSISENSLVAMDFS-GQKSRVIEN-----PTEALSVAVEEGLAWR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AGCGAM------QRLVSMGINIGSKLKVIRNQNGPVIISTKGSNIAIGRGLAMK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanobacterium.
Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococales;
Methanocaldococaceae; Methanocaldococcus.
NCBI_TAXID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein; Complete proteome.
SEQUENCE 82 AA; 8766 MW; 3F3810EEFC9F81CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Created)
01-027-1996 (Rel. 34, Last sequence update)
16-027-2001 (Rel. 40, Last annotation update)
Archaeal histone A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95138058; PubMed-7836329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 177:858-860(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U67505; AAB98558.1; -. TIGR; MJ0567; -.
                                                                                                                                                                                                                                                                                                                                                  Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methanobacterium formicicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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P48783;
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7
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 SPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQ 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 TPIKTWSRRSMITPEMIGHTFEV-HNGRKFLTVFVSETMVGHKLG-----EFSPTRMFK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine herpesvirus type 4 (strain 1942) (EHV-4) (Equine herpesvirus type 1 subtype 2).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirine; Varicellovirus.
NCBL_TAXID=10333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Whittaker G.R., Riggio M.P., Halliburton I.W., Killington R.A., Allen G.P., Meredith D.M.,
Allen G.P., Meredith D.M.,
"Antigenic and protein sequence homology between VP13/14, a herpes simplex virus type 1 tegument protein, and gp10, a glycoprotein of equine herpesvirus 1 and 4.";
Virol. 65:2320-2326(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: MODULATE ALPHA TRANS-INDUCING FACTOR-DEPENDENT
ACTIVATION OF ALPHA GENES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 10.0%; Score 42.5; DB 1; Length 88; Local Similarity 26.2%; Pred. No. 3.9e+02; es 16; Conservative 11; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
14 Dha trans-inducing factor 82 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                      Pfant PF00203; Ribosomal_819; 1.
PRINTS: PR00975; RIBOSOMALE319.
PRODOM: PD001012: Ribosomal_819; 1.
TIGREAMS: TIGR01050; rpsS_bact; 1.
FR053TE; PS00323; RIBOSOMAL_819; 1.
Ribosomal protein; rRRA-binding; Complete proteome.
SEQUENCE 88 AA; 10233 MW; ABB042B14E4C22F6 CRC64;
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Pfam; PF03387; Herpes_UL46; 1.
Transcription regulation; Trans-acting factor.
NON_TER 45 45
SEQUENCE 45 AA; 4862 MW. NABLEGATOR.
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                                                                                                                                                                                                                                                                                                                                           IPR002222; Ribosomal_S19.
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                                                                                                                                                                                                     EMBL; AE001323; AAC68125.1; -. EMBL; AE002347; AAF73605.1; -. HSSP; P60381; 10KF.
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000041;
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AC 0012_H
AC 0012_H
AC 01-DEC 01-DEC 01-DEC 01-DEC 01-DEC 01-DEC 01-DEC 02-DEC 02-
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                                       3;
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                                       18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., MayHew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPRANT-0157:H7 / EDL933 / ATCC 700927;
SPRANT-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                            25 MDFSGQKS--RVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSSATNMAI 79
                                                                                                                    1 MEASGSASWARVSKNLIERRAV------KGCL-----LPTPSDVMDAAVMAL 41
                                                                                                                                                                                                                                                                                                                                                             Escherichia coli, and
Escherichia coli 0157:H7.
Bacteria; Protecobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
           Length 45;
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78 AA; 8660 MW; 88976DE22CA9024B CRC64;
9.9%; Score 42; DB 1; 33.3%; Pred. No. 2e+02;
                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                      78 AA
                    Pred. No. 2e+0.
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MEDLINE-21156231; PubMed-11258796;
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                                                                                                                                                                                                                                                                                                                        Hypothetical protein yhgg.
YHGG OR B3410 OR 24765 OR ECS4252.
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EMBL; AE000416; AAC76435.1; --
EMBL; AE002563; AAG58511.1; --
EMBL; AP002565; BAB37675.1; --
EcoGene; EG12933; yhgG
                    Best Local Similarity 33.34
Matches 19; Conservative
                                                                                                                                                                                                                           STANDARD;
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Mau B., Shao Y.;
"The complete gen
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SEOUENCE 78
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P46845;
    Query Match
                                         Matches
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STRAIN-JF-1
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                        8; Gaps
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                                                                                                                                                                                                                                                                             8 SQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVE---EGLAWRKKGCLR 59
                                                              23 SQTLNTPQPMINAMLQQLESMGKAVRIQEEPDGCLSGSCKSCPEG-----KACLR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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  ) Db 1,
. 3.8e+02;
. . 3.8 21; Indels
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Score 42; DB 1; Lenge..
red. No. 4.1e+02;
-heg 19; Indels
 9.9%; Score 42; DB 1; Length 78;
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                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Toluene-4-monooxygenase system protein B (EC 1.14.13.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CVNRRVAPREGVMRVRKHRSTELFPRDMTIAESGL--NPTEVIDVVFEE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83 AA; 9457 MW; 4729FEF73F266F44 CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                           83 AA.
             llarity 27.3%; Pred. No. 3.8e-
Conservative 11; Mismatches
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9; Mismatches
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l Similarity 26.5%;
l3; Conservative
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                                                                                                                         STANDARD;
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                                                                                                                                                                                                     Pseudomonas mendocina.
           Local Similarity.
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Q00457;
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"Cloning and sequencing of Mycoplasma gallisepticum chromosome region
containing operons S10 and rrn255"."
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-- FOUCTION: PROFEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                               MEDLINE-95138058; PubMed-7836329;
Darcy T.J., Sandman K.M., Reeve J.N.;
"Methanobacterium formicicum, a mesophilic methanogen, contains three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                         J. Backeriol. 177:858-860(1995).

-! FUNCTION: BINDS AND COMPACT DNA (95 TO 150 BASE PAIRS) TO FORM NUCLEOSOME-LIKE STRUCTURES THAT CONTAIN POSITIVE DNA SUPERCOILS.

-! SUBUNIT: HOWODIMER OR HETERODIMER (POTENTIAL).

-! SIMILARITY: BELONGS TO THE HMF FAMILY OF ARCHARAL HISTOMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 IAPIGRIIKNA------GAERVSDDAREALAKALEE------KGETIATEAVKLAKHA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 ISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKG-----CLRLGTH- 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycoplasma gallisepticum.
Bacteria: Firmicutes: Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 41.5; DB 1; Length 67;
Pred. No. 3.6e+02;
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Last annotation update)
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Live 14; Mismatches
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InterPro; IPR004822; Histone_core.
Pfam; PF008008; CBFD_NFYB_HMF; 1.
DNA-binding; Multigene family.
SEQUENCE 67 AA; 7149 MW; 1132F83AG;
Methanobacteriaceae; Methanobacterium.
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30-MAY-2000 (Rel. 39, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 GRKTV--KASDVELAVKR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein S19.
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                                                                     SEQUENCE FROM N.A.
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                           NCBI_TaxID=2162;
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30-MAY-2000 (Rel
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Conservative
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-!- FUDMOTION: ELECTRON DONOR FOR PERIPLASMIC NITRATE REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 MRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSS 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 IKTWSRRSTIFPDFVGH-TFAVHNGKKFINVYVTEDMIGHKLG-----EFSPTRTFKGH 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saraiva L.M., Fauque G., Besson S., Moura I.;
"Physico-chemical and spectroscopic properties of the monohemic
cytochrome C552 from Pseudomonas nautica 617.";
Bur. J. Blochem. 224:1011-1017(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-007-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome c-552 (C552)
Marinobacter hydrocarbonoclasticus (Pseudomonas nautica).
Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
MARINOBACTER TOUDP; MARINOBACTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maras B., Schinina E., Di Leandro L., Pitari G., Malatesta F.; Submitted (NOV-2001) to the SWISS-PROT data bank.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                      Score 41.5; DB 1; Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- FUNCTION: ELECTRON DONOR FOR PERIPLASMIC NITRATE REDUCT-
-: SUBCELLULAR LOCATION: Periplasmic.
-:- PTM: BINDS ONE HEME GROUP PER MOLECULE.
-:- PTM: SINDLARIZER: MW-9466; METHOD-MALDI.
-:- SIMILARIY: BELONGS TO THE CLASS I CYTOCHROME C FAMILY.
PDB: ICNO; 22-JUL-99.
                                                                                                                                                                                                                                                                                                                                                                         Se+02;
                                                                                                 INTERPORT PROBLEZ REPOSOMBLES 
                                                                                                                                                                                                                                                                                                                                                                         23.8%; Pred. No. 5e+07
tive 14; Mismatches
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPR000345; Cytc_heme_bind.
InterPro: IPR000345; Cytc_heme_bind.
InterPro: IPR002329; Cyt_CIC.
Pfam: PR00034; CytcOthrome_c: 1.
ProDom; PR00405; CytCHROMECIC.
ProDom; PD004020; CytCHROMECIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95010061; PubMed-7925398;
                                                     EMBL; AF036708; AAB95391.1; -. HSSP; P80381; 10KF.
                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 23.8 es 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 ATN 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84 SSN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C552_MARHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-617
                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 16
C552_MARHY
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-ANSJOLOSES; PubMed-10684935;
MEDLINE-COLSOLOSES; PubMed-10684935;
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Lihher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Edhann M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Elsen J., Frasc C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 GQNGISQVPIYP-----NLAGQKE------QYLVAALKAYKAGQRQGQAPV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GRSGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CWL029, which is a state of the control of co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE $19P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
| PROSITE; PS00190; CYTOCHROME_C; 1. | PROSITE; PS00190; CYTOCHROME_C; 1. | PROSITE | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; DB'1; Length 88;
5e+02;
thes 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBL_TaxID=83558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0927R1; 09JRT8; 30-MR-2000 (Rel. 39, Created) 15-UNA-2000 (Rel. 41, Last sequence update) 15-UNA-2002 (Rel. 41, Last sequence update) 30S Tibosomal protein 319. RPSS OR RS19 OR CPN0643 OR CPN064.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5e+0
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=J138;
MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 THGSPTASSQSSATNMAIH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 MQGQATALSDADIANLAAY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.8%;
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TRAIN-ATCC 35092 / DSM 1617 / P2;

XRAIN-ATCC 35092 / DSM 1617 / P2;

XREAIN-ATCC 35092 / DSM 1617 / P2;

XREAIN-ATCC 35092 / DSM 1617 / P2;

XREDINE-2133296; Pubmed-11427726;

XREDINE-2133296; Pubmed-11427726;

XREDINE-2133296; Pubmed-11427726;

XREDINE-2133296; Pubmed-11427726;

XREDINE-2133296; Pubmed-1142726;

XREDINE-2133296; Pubmed-1142726;

XREDINE-2133296; Pubmed-1142726;

XREDINE-2133296; Pubmed-1142726;

XREDINE-2133296; Pubmed-1142726;

XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11420 - XREDINE-11
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {RNA}(N).
-!- SUBUNIT: THE S.ACIDOCALDIARUS RNAP IS COMPOSED OF 13 SUBUNITS.
-!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10
RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus solfataricus.
Archaeas (Tenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
Sulfolobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9.8%; Score 41.5; DB 1; Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5e+02;
hes 22; Indels
                                                                                                                                                                                                                                                           Pfam; PF00203; Ribosomal_S19; 1.
TIGRRAMS; TICRO1012; Ribosomal_S19; 1.
PROSITE; PS00323; RIBOSOMAL_S19; 1.
PROSITE; PS00323; RIBOSOMAL_S19; 1.
CONFLICT: 2 2 2 5 5 (IN REF 1)
SEQUENCE 88 AA; 10201 MW; EB1E98E3B4BC2588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 SPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 TPIKTWSRRSMITPEMIGHTFEV-HNGKKFLTVFVSETMVGHKLG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-UNV-2002 (Rel. 41, Last annotation update)
DNN-directed RNA polymerase subunit N (EC 2.77.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 26.7%; Pred. No. 5e+0
12; Conservative 10; Mismatches
                                                                                                                                                                                                                                       IPR002222; Ribosomal_S19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01194; RNA_pol_N; 1.
PROSITE; PS01112; RNA_POL_N_8KD; 1.
                                                                                           EMBL; AE001647; AAD18782.1; -. EMBL; AE02173; AAF73629.1; -. EMBL; AP002547; BAA98850.1; -. TIGR; CP0104; -. TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000268; RNA_pol_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE006647; AAK40429.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=2287;
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                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; euroside II; Brassicales; Caricaceae; Carica.
                                                                                                                                                                                                                        13 PMRSISENSLVAMDFSGQKSRVI--ENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASS 70
                                                                                                                                                                                                                                                          4 PIRCFICGSLIADKWQSFITRVNAGENPGKVL-----DDLGVKRYCCRRM------LLS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Walreavens V., Jaziri M., van Beeumen J., Schnek A.G., Kleinschmidt T., Looze Y.; Isolation and preliminary characterization of the cysteine-proteinases from the latex of Carica candamarcensis Hook."; Biol. Chem. Hoppe-Seyler 374:501-506(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40.5; DB 1; Length 43;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0cT-1993 (Rel. 27, Created)
01-0cT-1993 (Rel. 27, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Cysteine proteinase III (EC 3.4.22.-) (CC-III) (Fragment).
                                                                                                                                                     Length 66;
                                                                                                                                                              4.1e+02;
ches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                      ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
CO7748541A1CFA13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 AA; 4636 MW; F4C5D2881886E291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 EGLAWRKKGCL----RLGTHGSPTASSQSSAT---NMAIH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ESIDWRKKGAVTPVKNQGSCGSCWAFSTIATVEGINKIVH 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY CI. HSSP; P14080; 1YAL.
                                                                                                                                                   Score 41; DB 1;
Pred. No. 4.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR000668; Peptidase_C1.
Interpro; IPR001069; SHprot_acsite.
Pfan: Pr00112; Peptidase_C1; 1.
Probom; P0000158; Peptidase_C1; 1.
PROSITE; PS00649; THTOL_PROTEASE_HIS; PARTIAL.
PROSITE; PS00640; THTOL_PROTEASE_ASN; PARTIAL.
                                                                                                                                                            25.7%; Pred. www.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hydrolase, Thiol protease, Glycoprotein.
ACT_SITE 25 25 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Latex;
MEDLINE=94030669; PubMed=8216902;
                   Metal-binding; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GBG5_HUMAN STANDARD; P
P30670; Q61015;
01-APR-1993 (Rel. 25, Created)
                                                     10 10
44 44
45 45
66 AA; 7591 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.6%;
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                              71 QSSATNMAIHRSQP 84
                                                                                                                                                                                                                                                                                                                                 52 HVDIINEVIHYTRP 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carica candamarcensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ! - PTM: GLYCOSYLATED
                                                                                                                                                                  Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                            METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             CC3_CARCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
NON_TER
SEQUENCE
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                         METAL
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 19
CC3_CARCN
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                                                                                                                                                                                                                                                                                                                                                                                                                            PPECIES-Human; TISSUB-Blood;
MDDLINE-9818631; Pubmed-9653160;
MDDLINE-9818631; Pubmed-9653160;
Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
Wang Y.-X., Chen S.-J., Chen Z.;
Fund Y Genes expressed in human CD34(+) hematopoietic
Indentification of genes expressed in human CD34(+) hematopoietic
Stem/progenitor cells by expressed sequence tags and efficient full-
length CDNA cloning.";
Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBUNIT: G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).
-!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF TISSUES.
-!- MISCELLANEOUS: THERE ARE AT LEAST SEVEN DIFFERENT GAMMA SUBUNITS WITH POSSIBLE TISSUE-SPECIFIC DISTRIBUTION.
-!- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPTOG. DEV. 44:315-323(1996).
PUNCTION: GUANTINE NUCLEOTIDE-BINNING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODULATOR OR TRANSDUCER IN VARIOUS TRANSMEMBRANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE GTPASE ACTIVITY, FOR REPLACEMENT OF GDP BY GTP, AND FOR G PROTEIN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-Mouse; STRAIN-CF-1 / Harlan; Marbins-27011591; PubMed-8858601; Williams C-3., Schultz R.M., Kopf G.S.; Marliams C-3., Schultz R.M., Kopf G.S.; "G protein gene expression during mouse oocyte growth and maturation, and preimplantation embryo development."; Mol. Reprod. Dev. 44:315-323(1996).

-i- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE
01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Guanine nucleotide-binding protein G(I)/G(S)/G(O) gamma-5 subunit.
GNG5 OR GNGTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
SPECIES-Boxine, and Rat; TISSUE-Liver;
MEDLINE-92195304; PubMed-1549114;
Fisher K.J., Aronson N.N. Jr.;
"Characterization of the cDNA and genomic sequence of a G protein gamma subunit (gamma 5).";
Model Cell. 12:1585-1591(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Bovine; TISSUE-Spleen;
MEDILINE-93386792; PubMed-8326779;
MOTISHILE R., MSSUEM K., INVA M., KATO K., Asano T.;
"Identification of three forms of the gamma subunit of G proteins
                                                                                                                            Rattus norvegicus (Rtt), and
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606, 10090, 10116, 9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isolated from bovine spleen.";
Biochem. Biophys. Res. Commun. 194:1221-1227(1993).
                                                                                                                                                                                                                                                                                                MEDLINE-99009227; PubMed-9790912;
Liu B., Aronson N. N. Jr.;
"Structure of human G protein Ggamma5 gene GNG5.";
Biochem. Biophys. Res. Commun. 251:88-94(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES-Human; TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 8-53 FROM N.A.
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                                                                                         Homo sapiens (Human),
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
                                                                                                                                                                                                                                                                                 SPECIES-Human;
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: Cytoplasmic.
-i- ALTERNATIVE PRODUCTS: THE MEMBRANE ISOFORM ALPHA AND THE THREE CYTOPLASMIC ISOFORMS, BETA, GAMMA AND DELTA ARE GENERATED BY ALTERNATIVE SPLICING.
-i- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
BAX protein, cytoplasmic isoform gamma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 VKVSQAAADLKQFCLQNAQH-DPLLTGVSSSTN 57
                                                                                                           EMBL, AF085709; AAC72203.1; -...
EMBL, AF085708; AAC72203.1; JOINED.
EMBL, BC03855; AAC3869.1; -...
EMBL, M95779; AAA03563.1; -...
EMBL, M95779; AAA003563.1; -...
EMBL, U38780; AAA41188.1; -...
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TISSUE-B-cell;
MEDLINE-93364978; PubMed-8358790;
                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:109164; Gng5.
InterPro; IPR001770; G-gamma.
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                                                                                                                                                                                                                                                                                                                 PIR; JN0701; JN0701.
PIR; B42243; B42243.
Genew; HGNC:4408; GNG5.
                                                                                                                                                                                                                                                                                                                                                                                                         MIM; 600874;
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Q07815;
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BAXC_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *Accumulation of small heat shock proteins, including mitochondrial HSP22, induced by oxidative stress and adaptive response in tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant J. 13:519-527(1998).
-!- FUNCTION: MAY PLAY A PROTECTIVE ROLE AGAINST OXIDATIVE STRESS.
-!- SUBCELLULAR LOCATION: Mitochondrial.
-!- INDUCTION: BY HEAT SHOCK, AND UNDER OTHER CONDITIONS OF STRESS, SUCH AS INCREASED SALT CONCENTRATION AND STRAYATION.
-!- SIMILARITY: BELONGS TO THE SMALL HEAT SHOCK PROTEIN (HSP20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
16-DEC-1998 (Rel. 36, Last annotation update)
16-DEC-1998 (Rel. 36, Last annotation update)
16-DEC-1998 (Rel. 36, Last sequence update)
16-DEC-1998 (Re
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WEDLINE-98345975; PubMed-9680997;
Banzet N., Richaud C., Deveaux Y., Kazmaier M., Gagnon J.,
Triantaphylides C.;
                                                                                                                     Match 9.5%; Score 40; DB 1; Length 41; Local Similarity 31.0%; Pred. No. 3e+02; les 13; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thermoplasma acidophilum.
Archaea; Euryarchaeota: Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
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Pred. No. 4.4e+02;
4; Mismatches 10; Indels
MIM; 600040; -.
Apoptosis; Alternative splicing.
SEQUENCE 41 AA; 4678 MW; D94639AABB927859 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 AA; 6446 MW; 2AB9F927C7720076 CRC64;
                                                                                                                                                                                                                                                                                     1 MDGSG-----EQPRGGVSSRIEQGEWGGRHPSWPWTRCLRM 36
                                                                                                                                                                                                                                      25 MDFSGQKSRVIENPTEALSVAVEEG-----LAWRKKGCLRL 60
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
RPON OR TA0431.
                                                                                                                                                                                                                                                                                                                                                                                                                                               56 AA.
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PROSITE; PS01031; HSP20; PARTIAL.
Heat shock; Mitochondrion.
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9; Conservative
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                                                                                                                                                                                                                                                                  Nature 407:508-513(2000).
-!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10 .
RNA POLYMERASE SUBUNIT FAMILY.
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STRAIN-GSS1 / DSM 4299 / JCM 9571;

STRAIN-GSS1 / DSM 4299 / JCM 9571;

KWASHINE T. Amano N., Koike H., Makino S.-I., Higuchi S.,

KWASHINE T., Amano N., Koike H., Yamazaki M., Kanehori K.,

KWASHINE T., Yamano V., Watanabe K., Yamazaki M., Kanehori K.,

KWASHINE T., Yamanoto Y., Aramaki H., Makino K., Suzuki M.;

Archaeal adaptation to higher temperatures revealed by genomic
sequence of Thermoplasma volcanium.;

Sequence of Thermoplasma volcanium.;

Proc. Natl. Acad. Sci. U.S.A. 97:14257-14257(2000)

-I- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription

of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                           MEDLINE-20479972; PubMed-11029001; Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Meeves H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.
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PROSITE; PS01112; RNA_POL_N_BKD; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
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Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
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5,9e+02;
-hes 21; Indels
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ZINC (BY SIMILARITY).
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792AEDA20E5447E2 CRC64;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
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Pred. No. 9
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HSSP; O26147; 1EF4.
InterPro; IPR000268; RNA_pol_N.
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72 AA; 8368 MW;
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                                                                           -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10 RNA POLYMERASE SUBUNIT FAMILY.
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  substrates.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01194; RNA_pol_N; 1.
NSOSITE; RNS POL. MA. POL_NSED; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
Metal-binding; Complete proteome.
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Complete nucleotide sequence of bacteriophage T7 DNA and the
locations of T7 genetic elements.";
J. Mol. Biol. 166:477-535(1983).
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Pred. No. 7.9e+02;
8; Mismatches 8; Indels 1
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21-JUL-1986 (Rel. 01, Last sequence update)
01-YAR-1989 (Rel. 10, Last annotation update)
Gene 18.7 protein
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V187_BPT7

AC P03788;
DT 21-JUL-1986

DT 01-MAR-1989

DE Gene 18.7

OC T7-11ke vir

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                                         Mismatches
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                               Matches 15; Conservative
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                      61 GTHG 64
                                                                                                                                                                                                                                                                                                                                                                                              GKEG 64
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A;Gene: XFa0004
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A.Filte: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschil A; Reference number: A64300; MUID:96337999; PMID:8688087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this stable 58-kilobase pair plasmid is also designated ECL (large extrachromosd
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hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A.Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Reference number: A96039; MUID:21368234; PMID:11474104
A:Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-62 < BUL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Methanococcus jannaschii
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
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'Species: human immunodeficiency virus type 1, HIV-1

'Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999

'Accession: $24471; $24483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 VAPPKDLLDSTMSAADFA------QLFGVYTQGGMSWETFYERGQADGIFRLSGT 59
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A; Molecule V; ppe: DNA
A; Residues: 1-77 < SAL>
A; Cross-references: EMBL: Z11145; NID:g60073; PIDN:CAA77496.1; PID:g60074
C; Superfamily: AIDS-related virus gag polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein MJECL05 - Methanococcus jannaschii plasmid pURB800
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                                                                                                                                                                                                                                                                                                                                                                                    Length 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 RSISENSLVAMDFS-GQKSRVIENPTEALSVAVEEGLAWRKK 55
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A;Reference number: $24471
A;Accession: $24471
                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 22.18 es 15; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                            A; Genome: plasmid
                                                                                                                                                                                    C;Genetics:
A;Gene: SMa0736
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es 19; Conserv
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RiSimpSon, A.J.G.; ReindCh, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, F. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Frager, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.E.; Kitajina, J.P.; Krieger, J.B.; Kuramae, E.E.; Laiging, M.A.; Madeira, A.M.B.N.; Madeira, J.P.; Krieger, J.B.; Kuramae, E.E.; Laiging, M.A.; Madeira, A.M.B.N.; Madeira, M.P.; Marino, C.L.; Marques, M.; Martins, E.E.; Laiging, M.V.; Martins, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, M.C.; Palmieri, D.R. Rodrigues, V.; Rosa, A.J.; de Rosa A.T.; V.E.; de Sa, R.G.; Santelli, R.V.; Savasak A; Authors: all Silva, A.C.R.; de Silva, Silva, Jr.; W.A.; de Silvaira, M.A.; de Silvaira, M.A.; Salvaira, M.; Tsubako, M.H.; Vallada, H.; Van Silva, A.M.; Silva Jr.; W.A.; de Silvaira, M.F.; Tsubako, M.H.; Vallada, H.; Van Silva; W.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z.
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JC5345
Godd protein - Clostridium difficile
C;Species: Clostridium difficile
C;Species: Clostridium difficile
C;Species: Ostridium difficile
C;Date: 27-May-1997 #sequence_revision 18-Jul-1997 #text_change 15-Oct-1999
C;Date: 27-May-1997
C;Bate: 27-May-1997
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A;Residues: 1-81 <BRA>
A;Cross-references: EMBL:X92982; NID:g1770128; PIDN:CAA63566.1; PID:e212011; PID:g177013
C;Genetics:
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Ty25763
hypothetical protein F46FI1.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L3-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25763
R; Pauley, A.; Gattung, S.
Submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid F46FI1.
A;Refarence number: Z20083
A;Refarence number: Z20083
A;Refarence number: Z20083
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Retaus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-73 < PAUJ
A;Resi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
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tes 10; Conserv
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A;Map position: 1
A;Introns: 38/2
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Terredoxin 2[4Fe-45] - Methanosarcina thermophila
C;5pecies: Mathanosarcina thermophila
C;5decies: A42960
N;1decies: A42960
A; Reference number: A42960; MUID:92355496; PMID:1379583
A; Reference number: A42960; MUID:92355496; PMID:1379583
A; Residues: TM-1
A; Residues: TM-1
A; Residues: 1-60 <CLE>
A; Note: sequence extracted from NCBI backbone (NCBIN:110322, NCBIP:110324)
C; Genetics:
C; Reywords: 4Fe-45; electron transfer; iron-sulfur protein; metalloprotein
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C;Species: Ratus norvegicus (Norway rat)
C;Species: Ratus norvegicus (Norway rat)
C;Species: Ratus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: 153107; S25146
R;Shirasawa, T.; Aksahi, T.; Sakamoto, K.; Takahashi, H.; Maruyama, N.; Hirokawa, K.
Bsylirasawa, T.; Aksahi, T.; Sakamoto, K.; Takahashi, H.; Maruyama, N.; Hirokawa, K.
Bsylirasawa, T.; Aksahi, T.; Sakamoto, K.; Takahashi, H.; Maruyama, N.; Hirokawa, K.
A;Title: Gene expression of CD24 core peptide molecule in developing brain and develo
A;Title: Gene expression of CD24 core peptide molecule in developing brain and develo
A;Accession: 153107
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: mRNA
A;Residues: 1-76 cRES
A;Cross-references: EMBL:211663; NID:955901; PIDN:CAA77731.1; PID:955902
C;Keywords: phosphatidylinositol linkage
                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 CNQTSVAP-----RSGNQSISAAPNPTNATT-----RSGC-----55
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                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                              9 QSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTH 63
Score 45.5; DB 2; Pred. No. 3.8e+02; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 45; DB 2; Length 60; nilarity 42.9%; Pred. No. 3e+02; Conservative 7; Mismatches 9; Indels
                                                                                                                       8; Mismatches
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                            10.8%;
25.5%;
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                                                                                                                             14; Conservative
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Duggor expression/formation protein Hypc - Methanobacterium thermoautotrophic: Cippecies: Methanobacterium thermoautotrophicum Cippecies: Methanobacterium thermoautotrophicum Cippecies: Methanobacterium thermoautotrophicum Cipate: O5-Dec.1997 #sequence_revision 05-Dec.1997 #text_change 24-sep-1999 Cipate: D5-Dec.1997 #sequence_revision 05-Dec.1997 #text_change 24-sep-1999 Rishth, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, J. Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Mierzbowski, J.; Gibson, R.; Jiwar, M.; S.; Church, G.M.; Daniele, R.; Wang, Y.; Rice, P.; Noelling, J.; Reeve, J.N. A.Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H.; A.Accession: D69087 MID:98037514; PMID:9371463 A.Status; preliminary; nucleic acid sequence not shown; translation not shown A.Residues: 1-82 ATTHA A.CROSS-Teferences: GB:AED000224; GB:AED000666; NID:92622777; PIDN:ABB6122.1; PID:92 C.Genetics: A.Experimental source: strain Delta H. C.Genetics: A.Status preliminary A.M.CROSS-Teferences: GB:AED00054; GB:AED000666; NID:92622777; PIDN:ABB6122.1; PID:92 C.Genetics: MTH1649
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C.5pecies: Pisum sativum (garden pea (fragment)
C.5pecies: Pisum sativum (garden pea)
C.5pecies: Rendy A.M.; Watson, J.C.
Proc. Natl. Acad. Sci. U.S.A. 88, 6951-6955, 1991
A.7title: Differential accumulation of transcripts encoding protein kinase homologs
A.7ccession: C41139
A.7ccession: C41139
A.7ccession: C41139
A.7ccession: C41139
A.7ccession: C41139
A.7ccession: C58:M69032; NID:9169139; PIDN:AAA50774.1; PID:g169140
C.Superfamily: unassigned Sar/Thr or Tyr-specific protein kinases; protein kinase hc
C.5Keywords: plocyphotransferase
F:1-86/Domain: protein kinase homology (fragment) <KIN>
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 CYKADVSPIFEFSTNHKLHVDPLIVVSVIIDQKSRESVIAEFVAEPTIAFS----- 73
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 SGCNGCGMAPDLSYMEGSTTETLVMGVAPOKSHM---EASEMGVAAENG 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 10.6%; Score 45; DB 2; Length 82; Listiniarity 28.9%; Pred. No. 4.44-02; 11; Conservative 9; Mismatches 14; Indels
A; Residues: 1-79 <REI>
A; Cross-references: EMBL: U61973; NID:q1655850; PID:q1655851
A; Experimental source: apple flesh cortical tissue
C; Genetics:
                                                                                                                                                                                                                                                                                                         Match 10.6%; Score 45; DB 2; Local Similarity 30.6%; Pred. No. 4.2e+02; les 15; Conservative 7; Mismatches 21
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                                                                                                                                                      A;Gene: AMT1
C;Superfamily: metallothionein
C;Keywords: metal binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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A Cross-references: GB:AE001009; GB:AE000782; NID:92689332; PIDN:AAB89878.1; PID:9264926; Superfamily: hydrogenase expression/formation protein hypc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Species: Nelsectia menological purported] - Nelsectia meningitidis (strain MCSB serogroup of Species: Nelsectia meningitidis and settle 31-Mar-2000 #text_change 19-Jan-2001
Claccesion: DB146
R;Tettelin, H; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Hatt., D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Oin, H.; Vamathevan, J.; Jill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Attle: Complete genome sequence of Nelsecria meningitidis serogroup B strain MCSB. A;Seference number: All000; MUID:20175755; PMID:10710307
                                                                                                                                                           Rilenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, Fileischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L. A; Autubras: Utterback, T.; Cotton, W.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A;Reference umber: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein NMB0016 (imported) - Neisseria meningitidis (strain MC58 serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Cross-references: GB:AE002360; GB:AE002098; NID:g7225241; PIDN:AAF40495.1; PID:g722524
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Pysiol. Plantarum 100, 183-189, 1997
A;Title: Up-regulation of two cDNA clones encoding metallotthionein-like proteins in
A;Reference number: 218652
A;Accession: T17014
                 hydrogenase expression/formation protein (hypC) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999 C;Accession: H69420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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C;Species: Malus domestica (apple tree)
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 11-Jan-2000
C;Accession: T17014
R;Reid, S.J.; Ross. r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LVAMDFSGQKSRV----IENPTEALSVAVEEGLAWRK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 IAIVDFKGLKKEVRIDLLENPQIGDYVLVHVGMAIQK 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 TEALSVAVEEGLAWR--KKGCLRL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 TEWLPMSLRTGILWRFERKVCLEL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Best Local Similarity
Matches 10; Conserv
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A; Residues: 1-78 <TET>
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Query Match

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4;

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probable phage tail protein [imported] - Escherichia coli (strain 0157:H7, substrain Cispecies: Escherichia coli (species: Escherichia coli (species: Escherichia coli (species: 18-Jul-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #1-2001 #
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A; Residues: 1-78 <WHI>
A; Residues: 1-78 <WHI>
A; Residues: 1-78 <WHI>
B; Residues: 1-78 <WHI>
C; Cross-references: GB: AE001978; GB: AE000513; NID: g6459059; PIDN: AAF10892.1; PID: g645
A; Experimental source: strain R1
C; Genetics:
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: D85807
NT.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A;Fitle: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A65480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross references: GB:AE005174; NID:g12516000; PIDN:AAG56920.1; GSPDB:GN00145; UMGP:
A:Experimental source: strain 0157:H7, substrain EDL933
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: A75411
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R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A:Experimental source: strain 0157:H7, substrain RIMD 0509952
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C;Species: Deinococcus radiodurans
C;bate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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11arity 32.0%; Pred. No. 3.2e+02;
Conservative 6; Mismatches 11; Indels
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-78 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-51 <STO>
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Ay Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A; Reference number: AB1807; MUID:21595285; PMID:11759840
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D83807
Hypothetical protein 22988 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: 575293 S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996 A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-79 <KAN>
A; Residues: 1-79 <KAN>
A; Cross-references: EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA17207.1; PID:d101794
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                             periplasmic mercuric ion binding protein [imported] - Nostoc sp. (strain PCC 7120) C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 C; Accession: XB2271 XB271 X
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A; Residues: 1-64 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB75420.1; PID:g17132855; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
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hypothetical protein ssr2333 - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.
A;Variety: PCC 6803

C;Date: 25-Apr-1997 #text_change 08-Oct-1999

C;Date: 25-Apr-1997 #text_change 08-Oct-1999

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.5%; Score 44.5; DB 2; Length 64; 16.7%; Pred. No. 3.7e+02; ive 20; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.7e+02;
thes 17; Indels
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Best Local Similarity lb...
Best & Conservative
                                                                                         53 RKKGCLRLGTH 63
                                                                                                                                                        : | :|||
74 --RSC--VGTH 80
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A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: as13721
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AB2271
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Search completed: March 28, 2003, 09:09:01
Job time : 40.7323 secs
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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Tille: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gence A;Reference number: A99629; MOID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein Atu0630 [imported] - Agrobacterium tumefaciens (strain C58, Dupont) C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AH2653 C;Accession: AH2653 Asetubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   excisionase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509952)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: G90914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Status: preliminary
Abdocute type: DNA
A'Residues: 1-83 <HAY>
A'Cross-references: GB:BA000007; PIDN:BAB35710.1; PID:913361753; GSPDB:GN00154
A'Experimental source: strain 0157:H7; substrain RIMD 0509952
                                                                                                                              8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:X76604; NID:g471318; PIDN:CAA54065.1; PID:g471319
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                                                                                                                                                              21 SLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSSATN 76
                                                                                                                                                                                                     10 SLAAFDNGAMKKAVLAVPALLLALSL-----SGCQKQADSNTSTSTTTTKSTD 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 43.5; DB 2; Length 83; 22.2%; Pred. No. 6.6e+02; Live 10; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 87;
                                                                            Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 SISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGL 50
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                                                                    10.4%; Score 44; DB 2; 121.4%; Pred. No. 5.3e+02; tive 13; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43.5; DB 2;
Pred. No. 6.9e+02;
8; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.3%;
Best Local Similarity 34.1%;
Matches 14; Conservative
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 22.2%
Matches 12; Conservative
                                                                                             Local Similarity
ses 12; Conserv
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-87 <AAL>
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                        A; Map position: 1
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A;Gene: DR1317
                                                                       Query Match
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erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; Mc
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2233, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-*
                                                                                                                                                                   Afficie The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Afficie The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
Afficience number: AB2577; PMID:11743193
Afficience: AH2653
Afficience: AH2653
Afficience: Afficience AH2653
Afficience: Type: DNA
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Afficience: Afficience Strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 SGCSSQSISPMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTH 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 10.3%; Score 43.5; DB 2; Length 89; Best Local Similarity 26.2%; Pred. No. 71e+02; Anders Aatches 17; Conservative 9; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: circular chromosome
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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:

March 28, 2003, 09:08:20 ; Search time 27.1181 Seconds
 (without alignments)
181.900 Million cell updates/sec

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

237916 seqs, 58723674 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 40 Maximum DB seq length: 90

Maximum Match 100%

Listing first 1000 summaries

Listing first 1000 summaries

Listing first 1000 summaries

Published Applications April

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Section 1024	Codinance 1024 An	Sequence 1024, Ap	Sequence 47571 A	Sequence 6. Appli	Sequence 42490 A	Seguence 393. App	Sequence 218. Ann	Sequence 131. Ann	Sequence 131. Ann	Sequence 468. App	A	Sequence 700. Ann	Sequence 1460, Ap	Sequence 1460. An	Sequence 1372. An	Seguence 1437, An	Seguence 1493. An	Sequence 1528, Ap	
	ID	US-09-925-299-1024	US-09-925-299-1024	US-09-908-711-103	US-09-864-761-47521	US-10-125-258-6	US-09-864-761-42490	US-09-764-872-393	US-09-764-887-218	US-10-079-854-131	US-09-764-878-131	US-09-764-860-468	US-10-092-154-700	US-09-764-847-700	US-09-925-299-1460	US-09-925-299-1460	US-09-925-299-1372	US-09-925-299-1437	US-09-925-299-1493	US-09-925-299-1528	
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ф	Ouery Match	12.9	12.9	12.2	12.1	11.9	11.5	11.1	11.0	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	
	Score	54.5	54.5	51.5	51	50.5	48.5	47	46.5	46	46	46	46	46	45.5	45.5	45.5	45.5	45.5	45.5	
	Result No.	-	7	Э	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19	

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Sequence 134, App Sequence 134, App Sequence 131, App Sequence 131, App Sequence 131, App Sequence 132, App Sequence 132, App Sequence 1313, App Sequence 1513, App Sequence 1513, App Sequence 1513, App Sequence 1724, App Sequence 1724, App Sequence 1724, App Sequence 1724, App Sequence 132, App Sequence 133, App Sequence 134, App Sequence 1484, App Sequence 1484, App Sequence 1484, App Sequence 154, App Sequence 156, App Sequence 156, App Sequence 156, App Sequence 1894, App Sequ	
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (8)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (10)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAMEYKEY: SITE
LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAMEYKEY: SITE
LOCATION: (23)
LOCATION: (26)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (38).
2. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1024
                                                                   Gaps
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i Sequence 1024, Application US/09925299
i Sequence 1024, Application US/09925299
i Patent No. US2002005527A1
i GENERAL INFORMATION:
I TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
i TITLE OF INVENTION: Nucleic PA10
i CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
i PRIOR FILING DATE: 1999-03-12
i NUMBER OF SEQ ID NOS: 1556
i SOFFWARE: PATENTING DATE: 1999-03-12
i NUMBER OF SEQ ID NOS: 1556
i SEQ ID NO 1024
i LENGTH: 60
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| Patent No. US20020045230A1
| Patent No. US20020045230A1
| APPLICANT: Rosen et al. |
| TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PAL28
| CURRENT FILING DATE: 2001-07-20
| PRIOR PELING DATE: 2001-01-17
| PRIOR FILING DATE: 2001-01-17
| PRIOR FILING DATE: 2001-01-17
| PRIOR FILING DATE: 2001-01-17
| PRIOR PLING DATE: 2001-01-17
| PRIOR PAPLICATION NUMBER: 09/764,867
| PRIOR PAPLICATION NUMBER: US01/01344
12.9%; Score 54.5; DB 9; Length 60; nilarity 50.0%; Pred. No. 11; Conservative 1; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 12.9%; Score 54.5; DB 10; Length 60; Best Local Similarity 50.0%; Pred. No. 11; Matches 14; Conservative 1; Mismatches 12; Indels
                                                                                                                       58 LRLGTHGSPTAS-SQSSATNMAIHRSQP 84
                                                                                                                                                                                33 LELATXGDPPASASOSGGITGVSHRAQP 60
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R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 09/764,892

RR APLICATION NUMBER: 05/764,892

RR FILING DATE: 2001-01-17

R APPLICATION NUMBER: 05/764,888

R FILING DATE: 2001-01-17

R APPLICATION NUMBER: 05/764,905

R FILING DATE: 2001-01-17

R PELING DATE: 2001-01-17

R PELING DATE: 2001-01-17

R FILING DATE: 2001-01-17

R FILING DATE: 2001-01-17

R FILING DATE: 2001-01-17

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R R PELICATION NUMBER: 05/764,891

R R PELICATION NUMBER: 05/764,891

R R PLING DATE: 2001-01-17

R R PELICATION NUMBER: 05/764,891

R R PLING DATE: 2001-01-17

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R R PLING DATE: 2001-01-17

R PELICATION NUMBER: 05/764,891

R PELICATION NUMBER: 05/764,891

R PELICATION NUMBER: 05/764,809

R APPLICATION NUMBER: 05/764,809

R APPLICATION NUMBER: 05/764,809

PRIOR FILING DATE: 2001-01-7
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,905
PRIOR PELICATION NUMBER: 09/764,905
PRIOR PELICATION NUMBER: 09/764,905
PRIOR PELICATION NUMBER: 051/01329
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 051/01339
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,891
PRIOR PELICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,869
PRIOR FILING DATE: 2001-01-17
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PRIOR FILING DATE: 2001-01-17
PRIOR PELICATION NUMBER: 09/764,809
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,809
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 09/764,809
PRIOR PELING DATE: 2001-01-17
PRIOR P

TYPE: PRT ORGANISM: Homo sapiens

Page

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SCHERAL INCORRATION G.

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, Bavid R.

APPLICANT: Rank, Bavid R.

APPLICANT: RAnk, Bavid R.

APPLICANT: HANZel, David R.

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: AMOUNTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERENCE: AMOUNTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE OF INVENTION: HUMAN GENE: 2001-005-23

GURRENT APPLICATION NUMBER: US 60/180, 312

FRIOR FILING DATE: 2000-105-23

FRIOR FILING DATE: 2000-105-23

FRIOR FILING DATE: 2001-01-30

FRIOR FILING DATE: 2001-01
NAME/KEY: SITE
LOCATIONS: (25)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-908-111-103
                                                                                                                                                                                                                                                                9; Gaps
                                                                                                                                                                                                                                                                                                                                                                             15 RSISENSLVAMDF-SGQKSRVIENPTEALSVAVEEGLAWRKK------GCLRLGTHGS 65
                                                                                                                                                                            Ouery Match 12.2%; Score 51.5; DB 10; Length 83; Best Local Similarity 27.5%; Pred. No. 41; Matches 19; Conservative 8; Mismatches 33; Indels 9
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Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 PTASSQSSA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 PWGSSQASS 77
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US-09-864-761-47521
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APPLICATION NUMBER: US 60/180,312
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APPLICANT: Hanzel, David R.
APPLICANT: CAP. WEBSHENG
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE APPLICATION NUMBER: US/09/864,761
CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSSA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------TEALSVAV-----EEGLAWRKKG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 GOKARLLSRPLRGVSGKHCLTFFYHMYGGGTGLLSVYLKKEEDSEESLLWRRRG 64
                                                                                     OTHER INFORMATION: MAP TO ALL58153.2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.7
OTHER INFORMATION: EST. HUMAN HIT: BF573955.1, EVALUE 1.60e-02
OTHER INFORMATION: SWISSPROT HIT: Q91641, EVALUE 3.00e-25
US-09-864-761-47521
                                                                                                                                                                                                                                                                                          Query Match 12.1%; Score 51; DB 10; Length 84; Best Local Similarity 27.8%; Pred. No. 48; Matches 15; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Altier, Daniel J.
APPLICANT: Hermann, Rafeel
APPLICANT: Hermann, Rafeel
APPLICANT: Hermann, Rafeel
APPLICANT: Hou Albert L.
APPLICANT: Presnail, James K.
APPLICANT: Presnail, James K.
APPLICANT: Wong, James F. H.
TITLE OF INVENTION: Antimicrobial Polypeptides and Their
TITLE OF INVENTION: Antimicrobial Polypeptides
FILE REPRESENCE: 35718,246315
CURRENT FILING DATE: 2002-04-18
PRIOR PELICATION NUMBER: 2002-04-18
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 127
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH BOO G.
LENGTH BOO G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Indels
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28.8%; Pred. No. 51;
tive 10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 42490, Application US/09864761 Patent No. US20020048763A1 APPLICANT: Penen, Sharron G. APPLICANT: Renh, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/10125258 Publication No. US20030028920A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      29 GOKSRVIENP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 28.8 enes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Manduca sexta
                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: 78
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US-09-864-761-42490
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TYPE; PRT
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Gaps
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OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN HERAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PRAIN, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN PADLE ARROW, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN BOULE MARROW, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL = 3.9

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL = 3.9

OTHER INFORMATION: EXTREMAN HIT: BE272485.1, EVALUE 6.50e-30

US-09-864-761-42490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels
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PRIOR PELICATION NUMBER: US 60/20/0.456
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELICATION NUMBER: US 09/632,366
PRIOR PELING DATE: 2000-08-03
PRIOR PELING DATE: 2000-10-04
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2000-10-09
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/00663
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 09/774,203
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-20
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 09/774,203
PRIOR PELING DATE: 2001-01-20
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PERI
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1 Similarity 33.3%; Pred. No. 93;
15; Conservative 7; Mismatches
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2000-02-04
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Best Local Similarity
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Gaps
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Patent No. US20020094953A1

GENERAL IMPORMATION:

TILLE APPLICATW: ROSEn et al.

TILLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/764,860

CURRENT FILIKO DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER: OF SEQ ID NOS: 1198

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 468
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                                                                                                                                                                                                                                                                                                      APPLICANT ROSE at al.

ITILE OF INVERTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PAL21
CURRENT APPLICATION NUMBER: US/09/764,878
CURRENT FILLING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF EQO ID NOS: 428
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 68;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC009C1
CURRENT APPLICATION NUMBER: US/10/092,154
CURRENT FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 10.9%; Score 46; DB 10; Length 68. Best Local Similarity 47.4%; Pred. No. 1.44+07. Matches 9; Conservative 4; Mismatches 6; Indels Matches 9;
6; Indels
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                                                        9; Gaps
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                                                                                                                                                                                                                                                                Sequence 1460, Application US/09925299
Sequence 1460, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: NUCLEIC Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR PELICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PAtentIn Ver. 2.0
SEQ ID NO: 1460
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Publication No. US2003004061749
GENERAL INFORMATION:
TITLE OF INFORMATION:
TITLE OF INFORMATION: Nucleic Acids, Proteins and Antibodies
TITLE OF INFORMATION: NumBER: US/09/925,299
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR FILICATION NUMBER: PCT/USO0/05883
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 10.8%; Score 45.5; DB 10; Length 56; Best Local Similarity 35.4%; Pred. No. 1.3e+02; Matches 17; Conservative 6; Mismatches 16; Indels 5
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Match 10.8%; Score 45.5; DB 9; Length 56; Local Similarity 35.4%; Pred. No. 1.3e+02; les 17; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 NPTEALSVAVE--EGLAWRKKGC---LRLGTHGSPTASSQ----SSAT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37 NPTEALSVAVE -- EGLAWRKKGC -- - LRLGTHGSPTASSQ -- -- SSAT 75
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Matches 17; Conservative
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US-09-925-299-1460
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US-09-925-299-1372
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Gaps

6

us-09-936-697-6.max.rapb

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GENERAL INFORMATION:
APPLICANT Rosen et al.
TITLE OF INVENTOR:
TITLE OF INVENTOR: Notein and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CCT/US00/05882
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
STOR FILING DATE: 2000-03-08
STOR PALICATION NUMBER: 60/124,270
PRIOR PILING DATE: 2000-03-08
STOR PALICATION NUMBER: 60/124,270
PRIOR PILING DATE: 2000-03-08
STOR PALICATION NUMBER: 60/124,270
PRIOR PILING DATE: 1644
SOFTHARE: PALENTIN VET: 2.0
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Patent No. US20020055627A1
GENERAL INFORMATION 10200505627A1
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PCT/US00/05883
PRIOR PALICATION NUMBER: PCT/US00/05883
PRIOR PALICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
STORTOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SEQ ID NO 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.8%; Score 45.5; DB 9; Length 58; Best Local Similarity 35.4%; Pred. No. 1.38+02; Matches 17; Conservative 6; Mismatches 16; Indels.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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; Patent No. US20020052308A1
                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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Matches 17; Conservative
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US-09-925-299-1528
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; ORGANISM: Homo sapiens
US-09-925-301-1647
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LOCATER ION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1493
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FUBLication No. US20030040617A9
GENERAL INFORMATION NO. US20030040617A9
FILE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PALO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
FRIOR PRICATION NUMBER: PCT/US00/05883
FRIOR FILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SCOTWARE: PATCHTIN VOF. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.8%; Score 45.5; DB 9; Length 58; 35.4%; Pred. No. 1.3e+02; tive 6; Mismatches 16; Indels
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                                                        Sequence 1437, Application US/09925299
Publication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37 NPTEALSVAVE--EGLAWRKKGC---LRLGTHGSPTASSQ----SSAT 75
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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Matches 17; Conservative
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US-09-925-299-1437
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                                     -09-925-299-1437
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US-09-925-299-1493
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Gaps

Sequence 1528, Application US/09925299 Publication to US20030040617A9 GENERAL INFORMATION: APPLICANT: Rosen et al.

US-09-925-299-1528

Gaps

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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1493 APPLICATE Nosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO.
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 0CT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PILING DATE: 2009-03-08
PRIOR PILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 1493 Sequence 1493, Application US/09925299 Patent No. US20020055627A1 GENERAL INFORMATION: ORGANISM: Homo sapiens RESULT 23 US-09-925-299-1493 LOCATION:

Search completed: March 28, 2003, 09:19:20 Job time : 31.1181 secs

Length 58;

Score 45.5; DB 10; Pred. No. 1.3e+02;

10.8%;

Query Match Best Local Similarity

3 ä 9; Gaps Gaps 1; Gaps 9. APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILLNG DAPRE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1350
LENGTH: 60 / Match 10.8%; Score 45.5; DB 10; Length 5½; Local Similarity 35.4%; Pred. No. 1.3e+02; nes 17; Conservative 6; Mismatches 16; Indels 9 Sequence 1528, Application US/09925299
Fatent NO. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
FITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT APPLICATION NUMBER: PC7/0S00/05883
FRIOR FILING DATE: 2001-08-10
FRIOR PLILING DATE: 2000-03-08
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver: 2.0 10.8%; Score 45.5; DB 10; Length 60; 33.3%; Pred. No. 1.4e+02; tive 6; Mismatches 25; Indels 6; Mismatches 16; Indels 37 NPTEALSVAVE--EGLAWRKKGC---LRLGTHGSPTASSQ----SSAT 75 8 NPLVNLTVSPKRNSSLDTRKKPCRESKKFNTHSRPKSSHQLRKRSSST 55 37 NPTEALSVAVE--EGLAWRKKGC---LRLGTHGSPTASSQ----SSAT 75 6 PGQFFVFLVEMGFHHVGQAGLELLTSGDPPTSASQSAGITGMSHCAQP 53 38 PTEALSVAVEEGLAWRKKGCLRLGTHGS-PTASSOSSATNMAIHRSOP 84 Sequence 1350, Application US/09764877 Patent No. US20020147140A1 GENERAL INFORMATION: Conservative Matches 17; Conservative ; ORGANISM: Homo sapiens US-09-925-299-1528 ; ORGANISM: Homo sapiens US-09-764-877-1350 Local Similarity RESULT 25 US-09-764-877-1350 US-09-925-299-1528 Query Match LENGIH: 58 TYPE: PRT Query Match Matches Matches δ QQ

Gaps

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March 28, 2003, 09:03:25; Search time 24.4724 Seconds (without alignments) 100.992 Million cell updates/sec GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model Marting (1975) 18 (1975) 19 (1975) 1 Run on:

1 QGRSGCSSQSISPMRSISEN....SPTASSQSSATNMAIHRSQP 84

Seguence :

262574 segs, 29422922 residues Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

20297 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 40 Maximum DB seq length: 90

Post-processing: Minimum Match 10%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 18, Appl Sequence 611, App Sequence 20, Appl Sequence 20, Appl Sequence 111, Appl Sequence 113, Appl Sequence 173, Appl Sequence 173, Appl Sequence 5, Appl Sequence 2848, Appl Sequence 27, Appl Sequence 76, Appl Sequence 76, Appl Sequence 52, Appl Sequence 30, Appl Sequence 22, Appl Sequence 5, Appli Sequence 615, Appl Sequence 18, Appl Description US-09-100-804-30
US-09-311-936A-22
US-09-149-476-615
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US-09-149-476-611
US-09-27-357-611
US-09-27-357-111
US-09-27-117-12
US-09-27-117-12
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S171684-3
US-09-134-001C-2848
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US-09-134-001C-2848
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US-08-927-219-49
US-08-928-472-52 SUMMARIES % Query Match Length DB Score 45.5 45.4 44.5 42 42 42 41.5 40.5 40.5 40.5 40.5 43.5 43.5 43.5 43 43 Result

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4 US-08-469-260A-383 4 US-08-630-915A-134 5 US-08-177-294 5 US-08-177-294 5 US-08-203-806B-11 6 US-08-203-806B-11 7 US-08-203-806B-11 7 US-08-107-75A-11 7 US-08-107-75A-13 7 US-08-107-
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US-08-468-674B-73 Sequence US-08-780-571-73 Sequence US-08-780-571-73 Sequence US-08-736-44A-5 Sequence US-08-736-44A-5 Sequence US-08-736-44A-8 Sequence US-09-736-44A-8 Sequence US-09-736-44A-8 Sequence US-09-71-982-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-773-731A-2 Sequence US-08-773-74A-191 Sequence US-08-773-74A-191 Sequence US-08-773-74-74A-191 Sequence US-08-774-74A-193 Sequence US-08-774-774-74A-193 Sequence US-08-774-74A-193 Sequence US-08-774-74A-19	US-08-408-715 Sequence US-08-707-743 Sequence US-08-707-743 Sequence US-08-7127-289-3 Sequence US-08-7127-289-3 Sequence US-08-712-29-3 Sequence US-09-712-729-3 Sequence US-09-714-006-25 Sequence US-09-713-716-77 Sequence US-09-719-717 Sequence US-08-48-16-77 Sequence US-08-48-16-77 Sequence US-08-719-71-71 Sequence US-08-72-74-75-77 Sequence US-08-72-74-75-77 Sequence US-08-72-74-75-77 Sequence US-08-72-74-75-77 Sequence US-08-72-74-75-77 Sequence US-08-72-76-53 Sequence US-08-72-76-53 Sequence US-08-72-76-73 Sequence US-09-15-107-13 Sequence US-09-15-107-13 Sequence US-09-15-107-14 Sequence US-09-15-706-53 Sequence US-09-115-708-75 Sequence US-09-115-708-75 Sequence US-09-115-708-75 Sequence US-09-117-704-75
1 US-08-468-674B-73 Sequence 1 US-08-468-674B-73 Sequence 2 US-08-047-244-5 Sequence 2 US-08-049-244-5 Sequence 1 US-08-73-44-5 Sequence 1 US-08-73-44-25 Sequence 2 US-08-033-44-7-25 Sequence 4 US-09-134-011C-3226 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-193-59 Sequence 4 US-09-031-590A-3 Sequence 4 US-09-031-590A-3 Sequence 4 US-09-031-590A-3 Sequence 2 US-08-373-193-9 Sequence 2 US-08-373-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 4 US-08-660-726A-4 Sequence 4 US-08-660-726A-4 Sequence 4 US-08-673-403-403-403-403-403-403-403-403-403-40	1 US-08-708-71-75 Sequence 2 US-08-601-748-7 Sequence 2 US-08-61-908-19 Sequence 2 US-08-61-12-8908-19 Sequence 3 US-08-61-12-12-12-12-12-12-12-12-12-12-12-12-12
US-08-468-674B-73 Sequence US-08-780-571-73 Sequence US-08-780-571-73 Sequence US-08-736-44A-5 Sequence US-08-736-44A-5 Sequence US-08-736-44A-8 Sequence US-09-736-44A-8 Sequence US-09-736-44A-8 Sequence US-09-71-982-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-777-192-59 Sequence US-08-773-731A-2 Sequence US-08-773-74A-191 Sequence US-08-773-74A-191 Sequence US-08-773-74-74A-191 Sequence US-08-774-74A-193 Sequence US-08-774-774-74A-193 Sequence US-08-774-74A-193 Sequence US-08-774-74A-19	1 US-08-708-71-75 Sequence 2 US-08-601-748-7 Sequence 2 US-08-61-908-19 Sequence 2 US-08-61-12-8908-19 Sequence 3 US-08-61-12-12-12-12-12-12-12-12-12-12-12-12-12
1 US-08-468-674B-73 Sequence 1 US-08-468-674B-73 Sequence 2 US-08-047-244-5 Sequence 2 US-08-049-244-5 Sequence 1 US-08-73-44-5 Sequence 1 US-08-73-44-25 Sequence 2 US-08-033-44-7-25 Sequence 4 US-09-134-011C-3226 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-192-59 Sequence 2 US-08-377-193-59 Sequence 4 US-09-031-590A-3 Sequence 4 US-09-031-590A-3 Sequence 4 US-09-031-590A-3 Sequence 2 US-08-373-193-9 Sequence 2 US-08-373-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 2 US-08-33-476-80 Sequence 4 US-08-660-726A-4 Sequence 4 US-08-660-726A-4 Sequence 4 US-08-673-403-403-403-403-403-403-403-403-403-40	88 2 US-08-408-705 Sequence 88 2 US-08-408-71-75 Sequence 88 2 US-08-80-71-75 Sequence 90 3 US-08-80-71-75 Sequence 90 3 US-08-90-137-289-3 Sequence 90 3 US-08-91-27-289-3 Sequence 40 3 US-09-035-619-25 Sequence 40 3 US-09-514-006-22 Sequence 40 US-09-514-006-22 Sequence 40 US-09-514-006-22 Sequence 40 US-09-514-006-25 Sequence 41 US-09-514-006-25 Sequence 42 US-09-514-006-25 Sequence 43 US-09-514-006-25 Sequence 43 US-09-514-006-25 Sequence 44 US-09-514-006-25 Sequence 45 US-08-48-161-77 Sequence 45 US-08-48-161-77 Sequence 46 US-08-48-13-3-31 Sequence 46 US-08-48-5-96-31 Sequence 49 US-08-465-96-31 Sequence 49 US-08-465-96-31 Sequence 49 US-08-516-859-10-13 Sequence 49 US-08-516-859-10-13 Sequence 49 US-09-155-107-13 Sequence 50 US-09-155-107-13 Sequence 50 US-09-155-107-14 Sequence 50
7.1 78 1 US-08-468-674B-73 Sequence 7.1 78 1 US-08-468-571-73 Sequence 7.1 78 1 US-08-04-55 Sequence 7.1 79 1 US-08-04-5 Sequence 7.1 79 4 US-09-134-001C-3226 Sequence 7.1 80 4 US-09-134-001C-3226 Sequence 7.1 80 2 US-08-77-1946-10 Sequence 7.1 80 2 US-08-77-1946-10 Sequence 7.1 80 4 US-09-137-687-59 Sequence 7.1 80 4 US-09-137-192-59 Sequence 7.1 80 4 US-09-091-590A-3 Sequence 7.1 80 4 US-09-091-590A-3 Sequence 7.1 80 4 US-09-091-590A-3 Sequence 7.1 80 4 US-08-091-590A-3 Sequence 7.1 80 4 US-08-680-726A-84 Sequence 7.1 80 4 US-08-680-726A-84 Sequence 7.1 85 4 US-08-680-726A-84 Sequence 7.1 85 4 US-08-680-726A-84 Sequence 7.1 85 4 US-08-092-409-84 Sequence 7.1 86 4 US-08-09-082-409-84 Sequence 7.1 86 4 US-08-092-409-84 Seque	7.1 88 1 US-08-408-175 Sequence 7.1 88 2 US-08-408-175 Sequence 7.1 88 2 US-08-401-390B-19 Sequence 7.1 88 2 US-08-401-390B-19 Sequence 7.0 40 3 US-08-461-390B-19 Sequence 7.0 40 3 US-09-035-403-22 Sequence 7.0 40 3 US-09-031-4006-22 Sequence 7.0 40 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 43 2 US-08-48-101-77 Sequence 7.0 43 2 US-08-48-101-77 Sequence 7.0 43 2 US-08-38-33-31 Sequence 7.0 45 2 US-08-34-33-31 Sequence 7.0 45 2 US-08-465-965-31 Sequence 7.0 49 2 US-08-465-965-31 Sequence 7.0 49 2 US-08-08-29-18-38-5 Sequence 7.0 49 2 US-08-08-29-18-38-5 Sequence 7.0 49 3 US-08-09-20-39-18-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8
78 1 US-08-468-674B-73 Sequence 105-08-780-571-73 Sequence 78 2 US-08-087-244-5 Sequence 79 1 US-08-702-344-5 Sequence 79 1 US-08-702-344-5 Sequence 79 1 US-08-702-344-25 Sequence 79 1 US-08-703-4474-95 Sequence 79 4 US-09-134-0102-328 Sequence 80 2 US-08-703-746-10 Sequence 80 2 US-09-71-982-59 Sequence 80 2 US-08-703-746-10 Sequence 80 4 US-09-71-982-59 Sequence 80 4 US-09-71-982-59 Sequence 80 4 US-09-71-982-59 Sequence 81 3 US-08-703-71-12 Sequence 82 4 US-09-71-982-79 Sequence 83 3 US-08-703-71-12 Sequence 83 4 US-09-703-703-99 Sequence 83 4 US-08-703-703-99 Sequence 84 2 US-08-703-703-99 Sequence 84 2 US-08-703-703-99 Sequence 84 2 US-08-703-703-99 Sequence 84 2 US-08-703-703-99 Sequence 85 3 US-08-703-703-99 Sequence 85 4 US-08-703-703-703-99 Sequence 85 4 US-08-703-703-99 Sequence 85 4 US-08-703-703-703-99 Sequence 85 4 US-08-703-703-703-703-703-703-703-703-703-703	7.1 88 1 US-08-408-175 Sequence 7.1 88 2 US-08-408-175 Sequence 7.1 88 2 US-08-401-390B-19 Sequence 7.1 88 2 US-08-401-390B-19 Sequence 7.0 40 3 US-08-461-390B-19 Sequence 7.0 40 3 US-09-035-403-22 Sequence 7.0 40 3 US-09-031-4006-22 Sequence 7.0 40 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 42 4 US-09-031-4006-25 Sequence 7.0 43 2 US-08-48-101-77 Sequence 7.0 43 2 US-08-48-101-77 Sequence 7.0 43 2 US-08-38-33-31 Sequence 7.0 45 2 US-08-34-33-31 Sequence 7.0 45 2 US-08-465-965-31 Sequence 7.0 49 2 US-08-465-965-31 Sequence 7.0 49 2 US-08-08-29-18-38-5 Sequence 7.0 49 2 US-08-08-29-18-38-5 Sequence 7.0 49 3 US-08-09-20-39-18-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8-8

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26 DFSGQKSRVIENPTEALS-----VAVEEGLAWRK 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Caenorhabditis elegans
                     INFORMATION FOR SEQ ID NO: 30 SEQUENCE CHARACTERISTICS: LENGTH: 68 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                      LUPDCLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
NATI-SENSE: ...
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COMPUTER READABLE FORM:
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                                                                                                                                                   HYPOTHETICAL: N

HYPOTHETICAL: NO

HYPOTHETICAL: NO

JANUEL SENSE: NO

US-09-100-804-30
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      TELEX:
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Matches
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APPLICANT: SARS, JAN
APPLICANT: GLAESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: RYRIMARY STRCTURE AND FUNCTIONAL
TITLE OF INVENTION: RYRIESSION OF WOCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 23, Appl
Sequence 11, App.
                                                                                             Sequence
Sequence
Sequence
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Sequence
Sequence
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CURRENT APPLICATION DATA 87.89-100, 804
APPLICATION NUMBER: US/09/100,804
                                                                         US-08-332-638-12
US-08-6792-405-6
US-08-842-15
US-08-842-799-6
US-08-469-260A-552
PCT-US92-05532-4
PCT-US92-11458-6
                                                                                                                                                                                                                      US-07-700-5256 3
PCT-US92-03123 3
US-08-262-03123 3
US-08-262-773-199
US-08-262-773-199
US-09-131-750-27
US-07-998-003A-71
US-08-453-654A-71
US-08-453-655A-71
                                         5-08-188-228-12
5-08-332-643-12
5-08-332-638-12
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CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
FILING DATE: 01-SEP-194
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LO461/7003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
BEDIOM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/09100804 Patent No. 6066472 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: GATES, EDWARD R. RECISTRATION NUMBER: 31,616 REFERENCE/DOCKET NUMBER: LO4 TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASSACHUSETTS
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           617-720-2441
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US-09-100-804-30
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US-09-083-521-5
US-09-083-521-5
Sequence 5, Application US/09083521
Patent No. 6048970
GENERAL INFORMATION:
APPLICANT: Gegeler, Karl J.
APPLICANT: Gorley, Neil C.
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                    4;
                                                                                                                              14 MRSISENSLVAMDFSGQKSRVI----ENPTEALSVAVEEGLAWRKKGCLRL 60
                                                                                                                                                              / Match 10.8%; Score 45.5; DB 4; Length 73; Local Similarity 29.4%; Pred. No. 77; Indels as 10; Conservative 7; Mismatches 12; Indels
Query Match 11.8%; Score 50; DB 3; Length 68; Best Local Similarity 31.4%; Pred. No. 17; Matches 16; Conservative 11; Mismatches 20; Indels Matches 16; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/09331930A

Sequence 22, Application US/09331930A

GENERAL INFORMATION:
APPLICANT: ZIMMET PAUL Z.
APPLICANT: ZIMMET PAUL Z.
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
CURRENT APPLICATION NUMBER: US/09/331,930A

CURRENT PILING DATE: 1999-06-30

PRIOR PILICATION NUMBER: PCT/AU98/00902
PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: AU PP0117/97

PRIOR APPLICATION NUMBER: AU PP0323/97

PRIOR APPLICATION NUMBER: AU PP0323/97

PRIOR APPLICATION NUMBER: AU PP0323/97

WUMBER OF SEC ID NOS: 27

LENGURARE: PATENTIN OFF: 2.1

SEQ ID NO S: 27

LENGURH: 73
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10.6%; Score 45; DB 3; Length 76;
Best Local Similarity 24.4%; Pred. No. 95;
Matches 19; Conservative 10; Mismatches 15; Indels 34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 CSSQSISPWRSISENSLVAMDFSGQKS-RVIENPTEALSVAVEEGLAWRKKGCLRLGTHG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TVDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for windows/MS-DOS 6.2
APPLICATION NUMBER: US/09/083,521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT ENCRAPTION:

TITLE OF INVERTION:

FILE OF INVERTION:

FILE OF INVERTION: 186 Human Secreted proteins

FILE OF INVERTION: 186

CURRENT FILING DATE: 1998-109-108

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: 6C/040, 162

EARLIER FILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 6C/040, 336

EARLIER FILING DATE: 1997-03-07

                                                                                                                                                                                                             FILING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0527 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIAES: single
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EARLIER FILING DATE: 1997-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 615, Application US/09149476
Patent No. 6420526
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56 ---SSLQSTAGLLALSLS 70
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CLONE: 1216498
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US-09-149-476-615
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ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,583

ER FILING DATE: 1997-05-23

ER APPLICATION NUMBER: 60/047,617

ER APPLICATION NUMBER: 60/047,618

ER FILING DATE: 1997-05-23

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R FILING DATE: 1997-05-23
R RFILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047, 632
R APLICATION NUMBER: 60/047, 632
R APLICATION NUMBER: 60/043, 601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043, 580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 569
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 569
R FILING DATE: 1997-04-11
R R PLING DATE: 1997-04-11
R R PLING DATE: 1997-04-11
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R R PLING DATE: 1997-04-11
R R PLING DATE: 1997-04-11
R R PLING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 674
R R PLING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 674
R R PLING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043, 674
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R APPLICATION NUMBER: 60/043,672
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,315
R FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,313
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APPLICATION UNMBER: 60/056,886
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION UNBER: 60/056,630
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
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APPLICATION NUMBER:
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EARLIER PELICATION NUMBER: 60/056,812
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 199
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EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER APPLICATION NUMBER: 60/047,585
EARLIER APPLICATION NUMBER: 60/047,586
EARLIER APPLICATION NUMBER: 60/047,586
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EARLIER FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-05-23
EARLIER PAPLICATION NUMBER: 60/047,586
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER PILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
FILING DATE: 1997-05-23
FILING DATE: 1997-05-23
FILING DATE: 1997-05-23
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION UNDBER: 60,056,662
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60,056,872
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LICATION NUMBER: 60/047,599
ING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,632
FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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Gaps
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Patent No. 6271368
GENERAL INFORMATION
APPLICANT: LINFORMATION
APPLICANT: ECK, JURGE
APPLICANT: ZINKE, Holger
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CURRENT PILING DATE: 199-06-19
EARLIER RPILING DATE: 199-06-15
EARLIER RPILING DATE: 1995-06-25
EARLIER RPILING DATE: 1995-06-26
SARLIER RPILING DATE: 1995-06-26
SOFTWARE: PELING DATE: 1995-06-26
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Sequence 611, Application US/09227357
Patent No. 6342881
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
                                                                                                                                                         EARLIER FILITON DATE: 1997-082
EARLIER FILITING DATE: 1997-082
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-06-05
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,69
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/04,610
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER APPLICATION NUMBER: 60/061,060
                                                                                                                             TR APPLICATION NUMBER: 60/056,862
TR FILING DATE: 1997-08-22
TR FILING DATE: 1997-08-22
TR APPLICATION NUMBER: 60/056,908
TR FILING DATE: 1997-08-26
TR APPLICATION NUMBER: 60/066,908
TR FILING DATE: 1997-08-26
TR FILING DATE: 1997-08-27
TR APPLICATION NUMBER: 60/048,964
TR FILING DATE: 1997-09-05
TR FILING DATE: 1997-09-05
TR FILING DATE: 1997-09-05
TR FILING DATE: 1997-09-05
TR APPLICATION NUMBER: 60/056,884
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APPLICATION NUMBER: 60/056,909
                                                                APPLICATION NUMBER: 60/056,875
FILING DATE: 1997-08-22
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                                -08-22
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US-08-776-059-18
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Best Local S
Matches 11
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CURRENT APPLICATION NOBRE: US/09/227,357
CURRENT FILIAGE DATE: 1999-01-08
EARLIER FILIAGE DATE: 1999-07-07
EARLIER FILIAGE DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,910
EARLIER PILIAGE DATE: 1997-09-10
EARLIER PILIAGE DATE: 1997-09-10
EARLIER FILIAGE DATE: 1997-09-10
EARLIER FILIAGE DATE: 1997-09-10
EARLIER FILIAGE DATE: 1997-09-10
EARLIER FILIAGE DATE: 1997-09-10
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4 SGCSSQS-----ISPMRSISENSLVAMDFSGQKSR--VIENPTEALSVAVEEGLAWRKK 55
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PAPLICANT: Meng, Baozhong
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
                                                                                       10.4%; Score 44; DB'4; Length 63; 28.6%; Pred. No. 99; tive 10; Mismatches 27; Indels
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CORRESPONDENCE ADDRESS:
CORRESPONDENCE NIXON, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30
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CLASSIFICATION:
PRIOR APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
FILING DATE:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 30,727
REFERENCE/DOCKET NUMBER: 19603/1722
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 KSRVIEN--PTEALSVAVEEGLAWRK 54
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TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                       Conservative
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amino acid
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Best Local Similarity 50.09
Matches 13; Conservative
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CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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MOLECULE TYPE: protein

US-09-081-320-20
; TYPE; PRT
; ORGANISM: Homo sapiens
US-09-227-357-611
                                                                                          Query Match
Best Local Similarity
Matches 18; Conserva
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A CILING DATE: 03-APR-1996 CLASSIFICATION: 536
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41.4%; Pred. No. 94;
tive 8; Mismatches
                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 SISENSLVAMDFS-GQKSRVIENPTEALS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 TVNKGSLVALGFSDGQEAR----PEEILN 47
Sequence 111, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION: APPLICANT: SPARKS, Andrew B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/09267177 Patent No. 6287856 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNER
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 41.4%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 55 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-111
                                                                                                                                                                                                                                                                                                                                                                                                     New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03
                                                                                                                                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 11
US-09-267-177-12
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                            MESOLY 1

Sequence 20, Application US/09574141A

Fatent No. 6395490

Sequence 20, Application US/09574141A

Fatent No. 6395490

GENERAL INPORMATION:

APPLICANT: GONSALVes, Dennis

APPLICANT: GONSALVes, Dennis

TITLE OF INVENTION: RUCLEIC ACIDS, PROTEINS, AND THEIR USES

TITLE OF INVENTION: RUCLEIC ACIDS, PROTEINS, AND THEIR USES

CURRENT FILING DATE: 2000-05-18

PRIOR PLICATION NUMBER: 60/047,147

PRIOR PLICATION NUMBER: 60/069,902

PRIOR PLICATION NUMBER: 60/069,902

PRIOR PLICATION NUMBER: 09/081,320

PRIOR PLICATION NUMBER: 09/081,320

PRIOR PLICATION NUMBER: 09/081,320

PRIOR PLICATION NUMBER: 09/081,320

NUMBER OF SEQ ID NOS: 97

SOFTHARE: FRSELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09707780

Batent No. 6399308

GENERAL INFORMATION:

APPLICANT: Gonsalves, Dennis

APPLICANT: Meng, Bacabong

TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS

TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES

CURRENT APPLICATION NUMBER: US/09/707,780

CURRENT FILIAG DATE: 2000-11-07

PRIOR APPLICATION UMBER: 09/081,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 44; DB 4; Length 80; 50.0%; Pred. No. 1.4e+02; tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match , 10.4%; Score 44; DB 4; Length 80; Best Local Similarity 50.0%; Pred. No. 1.4e+02; Matches 13; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Rupestris stem pitting associated virus US-09-574-141A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) ORGANISM: Rupestris stem pitting associated virus US-09-707-780-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR PELICATION NUMBER: 09/081,320
PRIOR PELICATION NUMBER: 09/081,320
PRIOR PELING DATE: 1998-05-19
PRIOR PELING DATE: 1997-05-20
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR PELING DATE: 1997-12-17
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FREESEQ FOR Windows Version 4.0
LENGTH: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 KSRVIEN--PTEALSVAVEEGLAWRK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 KSRVIEN--PTEALSVAVEEGLAWRK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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US-09-707-780-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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RESULT 10 US-08-630-915A-111

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APPLICANT: SPARKS, Andrew B.
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: KAY, Brian K.
APPLICANT: McCONDAIL, Stephen J.
APPLICANT: POWLKES, Dana M.
APPLICANT: POWLYED: Stephen J.
APPLICANT: POWLYEPPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Poet, Steven E.
APPLICANT: Ritchie, Branson W.
APPLICANT: Ritchie, Frank D.
APPLICANT: Niagro, Frank D.
APPLICANT: Lukert, Phil D.
TITLE OF INVENTION: Vaccines against Circovirus Infections; FILE REFERENCE: 21099.0057
CURRENT APPLICATION NUMBER: 0S/09/267,177
CURRENT FILING DATE: 1999-03-12
EARLIER FILING DATE: 1999-03-13
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 55;
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New York
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ZIP: 10036-2711
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SIGNAL
LOCATION: -36..-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-630-915A-208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                            15; Indels 11; Gaps
                                                                                                                                   Ouery Match 10.3%; Score 43.5; DB 4; Length 74; Best Local Similarity 31.1%; Pred. No. 1.5e+02; Matches 14; Conservative 5; Mismatches 15; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.2%; Score 43; DB 2; Length 53; 33.3%; Pred. No. 1e+02; tive 2; Mismatches. 8; Indels
                                                                                                                                                                                                                                                                                                      36 ENPTEALSVAVEEGLAWRKKGCLRLGTHGSPTASSOSSATNMAIH 80
                                                                                                                                                                                                                                                                                                                                                     Diskette, 3.50 inch, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-726-306A-144

Sequence 144, Application US/08726306A

Patent No. 5958684

GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: unbech, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams, Ph.D., Kathleen M.
REGISTATION UNDERS: 34,380
REPERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-910
INFORMATION FOR SEO ID NO: 144:
SELERA: (617) 345-9111
INFORMATION FOR SEO ID NO: 144:
ELENA: (617) 345-9111
SELENA: (617) 345-9111
S
                  ; ORGANISM: beak and feather disease virus US-09-267-177-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: MordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-0ct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-0ct-1995
PRIOR APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-1916
FILING DATE: 01-1916
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-1910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 SRVIENPTEALSVAVEEGLAWRKKGCL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 173, Application US/09247155A Patent No. 6312922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
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Best Local Similarity 33.39
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STRANDEDNESS: single
TOPOLGGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ns
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US-09-247-155-173
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APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: POWLES, Dana M.
APPLICANT: POWLEL, Stephen J.
TITLE OF INVENTION: POLYPEPPIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : LOCATION: -26,-25,-24
; OTHER INFORMATION: Xaa = any one of the twenty amino acids
US-09-247-155-173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.2%; Score 43; DB 4; Length 84; 36.7%; Pred. No. 2.1e+02; tive 2; Mismatches 13; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
GENERAL INVOKATION:

GENERAL INVOKATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducqueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
TILE REFERENCE: GENSET.021A
CURRENY APPLICATION NUMBER: US/09/247,155A
CURRENY FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/004,121
EARLIER APPLICATION NUMBER: 60/008,1563
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-06-10
EARLIER FILING DATE: 1998-06-10
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 NPTEALSVAVEEGLAWRKKGCLRLGTHGSP 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 NPDHHSCLAV----SWEAAGCHGAGTQQSP 43
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1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/630,915A
03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 208, Application US/08630915A Patent No. 6309820 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 36.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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8; Indels
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                   8; Indels
                                                                                                                                                                                                                                                             APPLICANT: Debre, Patrice.
APPLICANT: Mossalay, Mohammed D
TITLE OF INVENTION.
WATURATION OF HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
STREET: 556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LEBYZEN, Hans
APPLICANT: ECK, Jurgen
APPLICANT: EK, Axel
APPLICANT: BAUR, Axel
APPLICANT: INVEX, HOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, version #1.25 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/07/781,248A FILING DATE: 19911230
                6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4-18065/A/DEB
                                                          12 SPMRSISENSLVAMDFSGQKSRVIENPTE 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 SPMRSISENSLVAMDFSGQKSRVIENPTE 40
                                                                                              1 APVRSLN----CTLRDSGQKSLVMSGPYE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 APVRSLN----CTLRDSGQKSLVMSGPYE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION UNBER: 6B 90103565
FILING DATE: 09-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/08776059B Patent No. 6271368
                                                                                                                                                                                                      Sequence 5, Application US/07781248A Patent No. 5246699 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: IKeler, Barbara J.
REGISTRATION NUMBER: 36,170
REFERENCE/DOCKET NUMBER: 4-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-277-3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-277-4306
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; FRAGMENT TYPE: N-terminal US-07-781-248A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.99
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 amino acids
                Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                         New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                   Summit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07901
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US-08-776-059-16
                                                                                                                                                                                     -07-781-248A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                         Ouery Match 10.0%; Score 42.5; DB 4; Length 61; Best Local Similarity 33.3%; Pred. No. 1.5e+02; Matches 10; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Debre, Patrice
APPLICANT: Mossalayi, Molammed D
TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42; DB 1; Length 40; Pred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Irving M. Fishman, CIBA-GEIGY Corporation 556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19910116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fishman, Irring M
REGISTRATION NUMBER: 30258
REFERNEC/COCKET NUMBER: 4-17921/+/DEB
TELECOMUNICATION INFORMATION:
TELEPHONE: 908-277-4832
                                                                                                                                                                                                                                                                                                                                                                                         9 QSISPMRSISENSLVAMDFSGQKSRVIENP 38
                                                                                                                                                                                                                                                                                                                                                                                                                   6 QTLYPFSSVTEEELNEFE-KGETMEVIEKP 34
"" INFORMATION:
"" (212) 869-8090
"ELEX: (212) 869-8090
"ELEX: (212) 869-804/9741
"" INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 and no acids
TYPE: and no acid
TYPE: and no acid
TOPOLOGY:
MOLECT:
         REFERENCE/DOCKET NUMBER: 1101-174 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90016254
FILING DATE: 24 JAN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/07641971B Patent No. 5236706 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.9%;
Best Local Similarity 37.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE: N-terminal US-07-641-971B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               908-277-4306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                         ; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-915A-208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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4; Gaps
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Query Match 99%; Score 42; DB 6; Length 84; Best Local Similarity 26.5%; Pred. No. 2.86+02; Matches 13; Conservative 9; Mismatches 19; Indels
                                                                                                                                                                     6 CSSQSISP-----MRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE 48
                                                                                                                                                                                                   :: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 NEW YORK AVE, NW, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/023,082A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KERATINOCYTE GROWTH FACTOR-2
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APPLICATION NUMBER: PCT/US95/01790
FILING DATE: 14-FEB-1995
FILING DATE: 14-FEB-1995
APPLICATION DATA: US 08/461,195
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/023,852 ·
FILING DATE: 13-AUG-1996
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...ж: US/09/023,082A
13-FEB-1998
N: 435
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FILING DATE: 23-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/910,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/039,045
FILING DATE: 28-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US 60/055,561
13-AUG-1997
                                                                                                                                                                                                                                                                                                                             Sequence 76, Application US/09023082A Patent No. 6077692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOORE, PAUL A.
COLEMAN, TIMOTHY A.
GRUBER, JOACHIM R.
DILLON, PATRICK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,688
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              JIMENEZ, PABLO
DUAN, D. ROXANNE
RAMPY, MARK A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MENDRICK, DONNA
ZHANG, JUN
NI, JIAN
                                                                                                                                                                                                                                                                                                                                                                                            STEVEN M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 13-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WASHINGTON
                                                                                                                                                                                                                                                                                                                                            NO. 607/05.
AI INFORMATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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5171684-3
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US-09-023-082A-76
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Patent No. 6380370
GENERAL INFORMATION: GENERAL Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
TITLE OF INVENTION: BLOCONVERSIONS CATALYZED BY THE TOULUENE
MONOXYGENASE OF PSEUDOMANAS MENDOCINA KR-1
CURRENT APPLICATION DATA:
PILING DATE: 28-SEP-1990
PRIOR PAPALICATION NUMBER: U$/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: 177,631
FILING DATE: 05-APR-1988
                                                                                                                                                                                                                                                                                                                                  Ouery Match 9.9%; Score 42; DB 4; Length 47; Best Local Similarity 30.8%; Pred. No. 1.2e+02; Matches 8; Conservative 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.9%; Score 42; DB 4; Length 78; Best Local Similarity 27.3%; Pred. No. 2.5e+02; Matches 18; Conservative 9; Mismatches 21; Indels
FILE REFERENCE: 674503-2003
CURRENT APPLICATION NUMBER: US/08/776,059B
CUBRENT FILING DATE: 1999-06-19
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
EARLIER FILING DATE: 1996-06-25
NUMBER: PAPLICATION NUMBER: 95109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT PILING DATE: 1998-08-13
PRIOR PLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2848
LENGTH: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2848
                                                                                                                                                                                                                                                                                                                                                                                                                      22 LVAMDFSGQKSRVIENPTEALSVAVE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | : |:||:|| | :|:|| 3 LTFMEAVNKKARVVKNEARFLLIAIQ 28
                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Saponaria officinalis
US-08-776-059-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-001C-2848
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;Patent No. 5171684
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Sequence 9, Application US/09246500B

Sequence 9, Application US/09246500B

Patent No. 623494

GENERAL INFORMATION:
APPLICATT H0911, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein-Associated Serine Protease Activity and Methods;
TITLE OF INVENTION: Using the Substrates
FILE REFERENCE: 24730-2204

CURRENT FILING DATE: 1999-02-08

CURRENT FILING DATE: 1999-02-08

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ij
                                                                                                                                                           Owery Match
9.7%; Score 41; DB 4; Length 51;
Best Local Similarity 28.2%; Pred. No. 1.8e+02;
Marches 11; Conservative 3; Mismatches 11; Indels 14; Gaps
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Patent No. 5811304
GENERATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF ENVENTION: Zinc Finger Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%; Score 41; DB 4; Length 76; 38.5%; Pred. No. 3.3e+02; tive 4; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                              12 SWRRAGCPYASLTSWCCPSRSCRSMTMSMPTSKPSSSLT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-UNN-1995
FLESSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 RLGTHGSPTAS -- SQSSATNMAIHRS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 KLGQYASPTAKRCCQDGVTRLPMKRS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Mouse C4a Anaphylatoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
        LENGTH: 51 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 38.55
Matches 10; Conservative
                                                                               ; MOLECULE TYPE: protein US-08-927-219-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CARBOHYD
; LOCATION: (66)...(68)
US-09-246-500B-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Diego
STATE: California
                                      TYPE: amino acid
TOPOLOGY: linear
                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92122
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US-09-246-500B-9
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US-08-459-568-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 9
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bell, Graeme I.

APPLICANT: Yemagata, Kazuya

APPLICANT: Yemagata, Kazuya

APPLICANT: Oda, Naohisha

APPLICANT: Kaisaki, Pamela J.

APPLICANT: Horikawa, Yukto

APPLICANT: Horikawa, Yukto

APPLICANT: Horikawa, Yukto

APPLICANT: Horikawa, Wikto

APPLICANT: Horikawa, Wikto

APPLICANT: Horikawa, Wikto

APPLICANT: Horikawa, Hukto

APPLICANT: Horikawa, Hukto

TITLE OF INVENTION: GENES HEPATOCYTE NUCLEAR FACTOR (HNF) 1 ALPHA, HNF-1BETA

MUMBER OF SEQUENCES: 147
                                                                                                                                                                                                                                                         Query Match 9.8%; Score 41.5; DB 3; Length 87; Best Local Similarity 19.3%; Pred. No. 3.4+02; Conservative 15; Mismatches 31; Indels 21; Gaps Matches 16; Conservative 15; Mismatches 32; Indels 21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             2::|: | :||: |: ||: || 2 VKAINSNYYLAMNKKGKLYGSKEFNNDCKLKERIEENGYNTYA----SFNWQHNGRQMY 56
                                                                                                                                                                                                                                                                                                                                                         14 MRSISENSLVAMDFSGQ-----KSRVIENPTEALSVAVEEGLAWRKKG---C 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: CONCULTENTLY HERWITH CLASSIFICATION: 435 entrolly Herwith PRIOR APPLICATION: 435 entrolly Herwith PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/029, 679 FILING DATE: 0.0-0CT-1996 PRIOR APPLICATION WUMBER: US 60/028, 056 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: B 60/025,719 FILING DATE: 10-5EP-1966 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/927,219
FILING DATE: Concurrently Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Arnold, White & Durkee P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARCD: 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 49, Application US/08927219
; Patent No. 6187533
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LRLGTHGSPTASSQSSATNMAIH 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 VALNGKGAPRRGOKTRRKNTSAH 79
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEPHONE: 202-371-2600
TELEPRAX: 202-371-2540
INPORMATION FOR SED ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 87 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 49: SEQUENCE CHARACTERISTICS:
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                                                                                                                                               10POLOGY: linear

MOLECULE TYPE: protein

US-09-023-082A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1/CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houston
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US-08-927-219-49
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TOPOLOGY:
US-08-516-859A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.6%; Score 40.5; DB 2; Length 66; Best Local Similarity 47.4%; Pred. No. 3.1e+02; Matches 9; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.6%; Score 40.5; DB 2; Length 66; Best Local Similarity 47.4%; Pred. No. 3.1e+02; Matches 9; Conservative 7; Mismatches 2; Indels
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Sequence 52, Application US/08399411
Sequence 52, Application US/08399411
Sequence 52, Application US/08399411
Sequence 52, Application US/08399411
SEQUENTIAL INFORMATION:
TITLE OF INVENTION: Retinoblastoma Protein - Interacting TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: US-MAR-1995
CLASSIFICATION: 530
ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMUNICATION INFORMATION:
TELECOMUNICATION (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARRATERSFICS:
TENCTH. 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Campbell and Flores
STREEF: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                      FILING DATE: 05 WAR 1995

ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

RECISTRENEL/DOCKET NUMBER: P-LJ 1264

FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-901
TENGTH: 66 amino acid
TYPE: mino acid
APPLICATION NUMBER: US 08/399,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .... ERISTICS: 6.0 mino acids TYPE: amino acids ;
US-08-399-411-52 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 SISENSLVAMDFS-GQKSR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 TVNKGSLVALGFSDGQEAR 40
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Gaps
RESULT 25
US-08-516-859A-52
Sequence 52, Application US/08516859A
Sequence 52, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: A370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.6%; Score 40.5; DB 3; Length 66; 47.4%; Pred. No. 3.1e+02; tive 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                     STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STAFE: California
ZONNTR: USA
ZIE: 93122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
COMPUTER: IBM FC Compatible
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: USAGE 1995
CLASSIFICATION: 514
PROOF APPLICATION BATE
PRIOR APPLICATION DATA:
PELING DATE: 06-MRR.1995
FILING DATE: 06-MRR.1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-MG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: P-LJ 1776
TELEPHONE: (619) 535-9901
TELEPHONE: (619) 535-894
INFORMATION PROMATION:
TELEPHONE: (619) 535-894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/516,859A FILING DATE: 18-AUG-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-LJ 1776
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Job time : 32.4724 secs
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Best Local Similarity 47.4%
Matches 9; Conservative
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GY: linear
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March 28, 2003, 08:55:25; Search time 66.1417 Seconds (without alignments)
169.228 Million cell updates/sec
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Listing first 1000 summaries

2. SIDS2/gcdata/geneseq/geneseqp-embl/AA1981 DAT: 4
2. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
3. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
4. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
5. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
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6. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
7. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
8. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
91. SIDS2/gcdata/geneseqy-embl/AA1981 DAT: 4
10. SIDS2/gcdata/geneseqy-embl/AA1991 DAT: 4
11. SIDS2/gcdata/geneseqy-embl/AA1991 DAT: 4
12. SIDS2/gcdata/geneseqy-embl/AA1991 DAT: 4
13. SIDS2/gcdata/geneseqy-eneseqy-embl/AA1991 DAT: 4
14. SIDS2/gcdata/geneseqy-eneseqy-embl/AA1991 DAT: 4
15. SIDS2/gcdata/geneseqy-eneseqy-embl/AA1991 DAT: 4
16. SIDS2/gcdata/geneseqy-eneseqy-embl/AA1991 DAT: 4
17. SIDS2/gcdata/geneseqy-eneseqy-embl/AA1991 DAT: 4
18. SIDS2/gcdata/geneseqy-eneseqy-enebl/AA1999 DAT: 4
18. SIDS2/gcdata/geneseqy-eneseqy-enebl/AA1999 DAT: 4
19. SIDS2/gcdata
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                                                                                                                                                                                                                                                                                                                                                                             1 QGRSGCSSQSISPMRSISEN.....SPTASSQSSATNMAIHRSQP
                 GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0:5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 40 Maximum DB seq length: 90
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Query
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
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Peptide derived fr Peptide derived fr Peptide derived fr Peptide derived fr Human polypeptide Human polypeptide Human polypeptide Novel human diagno Human polypeptide
Nowel human secret
Human polypeptide
Human secreted pro
Human secreted pro
Human secreted pro
Human secreted pro
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AMB1895
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AMO2212
AMO0235
AMO1325
AMO1325
AMO1122
AMO1122
AMO1122
AMO1122
AMO10338
AMO10414
AMO10613
AMO10633

ABGG1744
AABC01560
AAO0895728
AAO085726
AAO08594
ABG47266
AAAO034736
AAAO034736
AAAO034034736
AAAO02479
AAAO02678
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ALIGNMENTS

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Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
AAB18942 standard; peptide; 84 AA.
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08-FEB-2001 (first entry)

Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.

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Homo sapiens
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21-SEP-2000

14-MAR-2000; 2000WO-FR00613. 99FR-0003159. 15-MAR-1999; (CNRS ) CNRS CENT NAT RECH SCI.

Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;

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ö
                                                                                                                                                            B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PFR-SHZ (STC homology 2) domains of a GFD7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SHZ (which by Itself is inactive). Agents that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, and syndrome X.
                                                 Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity
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RESULT 2 AAB18938

AAB18938 standard; peptide; 84 AA. AAB18938;

Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein. 08-FEB-2001 (first entry)

Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.

Rattus sp.

WO200055634-A1. 21-SEP-2000.

14-MAR-2000; 2000WO-FR00613.

99FR-0003159. 15-MAR-1999;

Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J; (CNRS ) CNRS CENT NAT RECH SCI.

WPI; 2000-587566/55.

Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity

Claim 2; Page 23-24; 46pp; French.

B18937-64 represent the PIR (phosphorylated insulin receptor interacting

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Conservative
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                                                        Local Similarity
es 43; Conserv
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Best Local Similarity
Matches 40; Conserv
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                      43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burnol A,
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                       Sequence
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                                                 Query Match
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region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Against that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases the winto insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome X.
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                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                     Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
                                                                                                                                                                               n 91.3%; Score 386; DB 21; Length.84;
Similarity 88.1%; Pred. No. 3.9e-42;
74; Conservative 5; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                      AAB18941 standard; peptide; 43 AA.
                                                                                                                                                                                                                                                                                                          61 GTHGSPTASSQSSATNMAIHRSQP 84
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                                                                   Gaps
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   Length 43;
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                                                                   indels
                                                                                                                                  13 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 55
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100.0%; Pred. No. 5.3e-20;
iive 0; Mismatches 0;
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Pred. No. 4.3e-19;
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RESULT 7
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                                                                                                  Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.
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                                                                                                                                                                                                                                                                                                              Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;
                                                                          Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
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Pred. No. 6.9e-17;
8; Mismatches 17;
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AAB18954 standard; peptide; 80 AA.
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SIZ (Src homology 2) domains of a Grb7 family protein. PIR sit he actual binding region but its effect is about 10 times greater in presence of SIZ (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases that that are potentially useful for treating insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome and syndrome X.
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diabetes; obesity; polycystic ovarian syndrome; syndrome X.
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Query Match
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR SIZ (Stc homology 2) domains of a Gtb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that effect binding between the peptides and the insulin receptor can talmulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases. Particularly diabetes and obesity but also polycystic ovarian syndrome
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Pred. No. 3.2e-16;
6; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                   44.0%; Score 2. Se-154.1%; Pred. No. 3.2e-1.
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Claim 2; Page 28; 46pp; French.
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peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome and syndrome X.
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                                                                                                                                                                                                                                                                                                                                                             4; Gaps
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                                                                                                                                                                                                                                                                                        Length 80;
                                                                                                                                                                                                                                                                                                                                                         17; Indels
                                                                                                                                                                                                                                                                                Score 179; DB 21;
Pred. No. 2.5e-15;
8; Mismatches 17;
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Best Local Similarity 59.2%;
Matches 42; Conservative
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Score 169; DB 21; Length 43; Pred. No. 2e-14;

40.0%; 76.7%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                   Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.
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                             13 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 55
                                                13 PMRSISENSLVAMDESGQKSRVIENPTEALSVAVEEGLAWRKK
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times affect binding between the peptides and the insulin receptor can that stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases that are potentially useful for treating insulin resoluting agents that are potentially useful for treating insulin-associated diseases.

Particularly will diabetes and obesity but also polycystic ovarian syndrome
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                                               Phosphorylated insulin receptor interacting region; Grb7 family protein insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.
                                                                                                                                                                                                                                                                                                                                                                           Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity
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                Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
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-kas 6; Indels
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SIZ (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SHZ (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, and syndrome X.
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                                            (CNRS ) CNRS CENT NAT RECH SCI.
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                99FR-0003159
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                                                                                                        WPI; 2000-587566/55
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nes 30; Conserv
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                15-MAR-1999;
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Gaps

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14-MAR-2000; 2000WO-FR00613.

21-SEP-2000.

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA01910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodilatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                       13 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 55
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                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 16107.
                                                                                                                                                                                                                                                                                                      AAO02215 standard; Protein; 47
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18-MAY-2000; 2000US-0577409
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es 30; Conserv
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inflammation.
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                B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Stc homology 2) domains of a GFD7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases particularly diabetes and obesity but also polycystic ovarian syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cencer; leukaemia; nervous system disorders; arthritis; inflammation.
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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity is activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomolary; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO and tip. Wipo int/pub/pub/shed_pct_sequences.
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                                                                                                                                                       Gaps
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                                                                                                                  Length 47;
                                                                                                                                                                             4;
                                                                                                                                                     Indels
                                                                                                               DB 22;
                                                                                                                                                  13;
                                                                                                                                                                                        48 EGLAWRKKGCLRLGTHGS---PTASSQSSATNMAIHRSQ 83
                                                                                                                                                                                                                4 DGVPWRNPGSLQPPSPGSSDPPTSASQESGTTGAHHHTR 42
                                                                                                               Score 65.5; Di
Pred. No. 0.6;
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human polypeptide SEQ ID NO 27451.
                                                                                                                                                                                                                                                                                                                         AAO13559 standard; Protein; 77 AA
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ilarity 38.5%;
Conservative 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-514838/56.
                                                                                                                                   Similarity
                                                                          47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200164835-A2.
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Length 77;

14.4%; Score 61; DB 22;

Query Match

(first entry)

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Human; chromosome mapping; gene mapping; gene therapy, forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                           Novel human diagnostic protein #7911.
                                                                ABG07920 standard; Protein; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
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                                                                                                                                                                                                                                                                                                                                                                               WO200175067-A2.
                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                 11-OCT-2001,
                                                                                                                  ABG07920;
                RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymoleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinial activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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                                      Gaps
                                      4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 23842; 1399pp + Sequence Listing; English.
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                              17; Indels
                                                                     40 EALSVAVEEGLAWRKKGCLRLGTHGS---PTASSQSSATNMAIH 80
                                                                                                         18 QSCSVAQARG-QWYNHGSLQPSTHGASNPPTSASQSVGTTGMSH 60
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8; Mismatches 13;
     38.6%; Pred. No. 4.7; tive 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                          Human polypeptide SEQ ID NO 23842.
                                                                                                                                                                                                                                         . AAO09950 standard; Protein; 76 AA.
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18-MAY-2000; 2000US-0577409
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Best Local Similarity 38.6
Matches 17; Conservative
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Matches 15; Conservative
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N-PSDB; AAI89881
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                                                                                                                                                                                                                                                                                         AA009950;
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The invention relates to isolated polynuclectide (I) and colypeptide (II) sequences. (I) is useful as hybridisation probes, colypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain receivable in the complaint of (II). The and gene mapping, and in recombinant production of (II). The colynuclectides are also used in diagnostics as expressed sequence tags (por identifying expressed genes. (I) is useful in gene therapy techniques (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or another in the polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful in medical contains in the polypeptide and polynucleotide sequences have applications in capture types of date and products dependent on DNA and confine acid sequences. ABG00010-ABG30377 represent novel human call sequences and products dependent on DNA and diagnostic amino acid sequences of the invention.

Confine and confine and confine and products dependent on DNA and confine and and sequences of the invention.

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Confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and confine and conf
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42.5%; Pred. No. 5.4;
:ive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; SEQ ID No 38279; 103pp; English.
      Tang YT;
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Drmanac RT, Liu C,
                                                                                                         WPI; 2001-639362/73.
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Best Local Similarity
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                                                                                                                                                                 N-PSDB; AAS72107
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RESULT 19 AAO11222

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Gaps

Indels

39 TEALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSSAT 75 

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, accines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
  Human, cytokine; cell proliferation, cell differentiation, gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
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stem cell proliferation; haemacopoiesis; nerve tissue regeneration;
immune suppression; immune stimulation; anti-inflammatory; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU30892 standard; Protein; 72 AA.
                                                                                                                                                                                                                                                                                                                                       Pang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                              28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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                                                                                                 Homo sapiens
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                                                                                                                                                                        07-SEP-2001.
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        The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynecleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activity to the coll and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                              Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 25114; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Score 58.5; DB 22; Length 78; 36.4%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 EALSVAVEEGLAWRKKGCLRLGTHGSPTASSQSSATNMAIHRSQ 83
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                                                                                                              Human polypeptide SEQ ID NO 25114.
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AA011222 standard; Protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                        28-FEB-2000; 2000US-0515126
18-MAY-2000; 2000US-0577409
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Conservative
                                                                        06-NOV-2001 (first entry)
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es 16; Conserva
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                                                                                                                                                                                                                                                                              WO200164835-A2.
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                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                07-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders
                                      AA011222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAO04576;
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05-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                     WPI; 2002-010886/01.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 AA;
            WO200177137-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200218412-A1.
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                                                    18-OCT-2001.
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                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predsposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells capressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptides and cells genetically englineered to express them are also useful for producing the proteins. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in the polypeptide and cells genetically and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopolesis; and in the polypeptide and/or stimulation; as anti-inflammatory agents; and in treatment of leukamains. Auguspilo Abanasa of the invention.
                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 SQSISPMRSISENSLVAMDFSGQKSRV-----IENPTEALSVA----VEEGLAWRK 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 SSSTNPLSSXXLNKIPSLPSSWEKWXIPPKNNCLSLLNPSPP-SLAPSLDDIKEGLSWKK 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albumin fusion protein; therapeutic protein X; human albumin; HA; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; endocrine disorder; haematopoleitc disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunemodulator; anti-HV; antidiabetic; haemostatic; nootropic; neuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%; Score 56; DB 22; Length 72; 27.9%; Pred. No. 19; tive 14; Mismatches 16; Indels
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                                                                                                                                                                                         Liu C, Drmanac RT;
                                        16-APR-2001; 2001WO-US08656.
                                                                               18-APR-2000; 2000US-0552929.
26-JAN-2001; 2001US-0770160
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                                                                                                                                                (HYSE-) HYSEQ INC.
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Synthetic.
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25-OCT-2001
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Human secreted protein; autoimmune disease; hyperproliferative disorder; cardiovascular disorder; carderioractular disorder; cancer; cancer; cancer; cancer; cancer; cancer; carder disorder; epithelial cell proliferation; wound healing; skin aging; sunburn; transplantation; chemotaxis; tissue regeneration; food additive; preservative; cytostatic; cardiant; antivallergic; antihflammatory; antibacterial; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shalf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and dispinsosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. alabtes), heamatopoietic disorders, mental disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). Abd63326-Abd665518 represent albumin
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                                                                                                                                                                                                                                                                                                                                                New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein - \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1828-1829; 2102pp; English.
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                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                      25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
                                                        12-APR-2000; 2000US-229358P.
12-APR-2001; 2001WO-US11988.
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Birse CE, Shi Y, Ch

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The present invention relates to the isolation of novel human secreted proteins and the polynucleotide sequences encoding them. The secreted proteins are useful to prevent, tread to amedicate encodical condition.

The e.g. humans, mice, rabbits, goats, horses, cats, doss, chickens or sheep. The secreted proteins are also useful in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the secreted proteins are also useful in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the secreted proteins and iso be used in also that associated with disorders and in diagnostic immunosasys e.g. radioimmunosasys or enzyme linked immunosorbent assays (ELISA). Disorders which can be arthitis, hyperpoliferative disorders e.g. cancer, cardioimscassular disorders e.g. cardiac arrest, cardioimscascular disorders e.g. cardiac arrest, cardioim disorders e.g. cardiac disorders e.g. parkinson's coular disorders e.g. corneal infection. The polypeptides can also be used to alm wound healing and epithalial call proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for sunburn, to maintain organs before transplantation, concommentally the polypeptides can also be used as a food additive or concommental purpose or decrease storage capabilities.

Augilo81-Augilu8 represent human secreted protein sequences.
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                                                                                                                                                                                                                                           Seventeen nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immun disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 56; DB 23; Length 79; illarity 39.3%; Pred. No. 22; Conservative 3; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                               Claim 11; Page 478-479; 505pp; English.
                                                                                           Komatsoulis GA, Baker KP,
Wei P, Ebner R, Duan RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 CLSIGQHELPSYSCQPGRKRLLPHHSQP 72
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                                             (HUMA-) HUMAN GENOME SCI INC.
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04-JAN-2001; 2001US-259516P.
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N-PSDB; ABK54162.
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es 11; Conserva
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                                                                                         Rosen CA,
Moore PA,
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AAO00883
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Gaps

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, heematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomcdulatory; cencer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                          Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
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                                                                                                                                                                                                                                            Claim 20; SEQ ID NO 14775; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 EGLAWRKKGCLRLGTHGS---PTASSQSSATNMAIHRSQ 83
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                                                                                        Fang YT, Liu C, Drmanac RT;
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28-FEB-2000; 2000US-0515126.
18-MAY-2000; 2000US-0577409.
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18-MAY-2000; 2000US-0577409.
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Best Local Similarity 33.3%
Matches 13; Conservative
                                                                                                                       WPI; 2001-514838/56.
N-PSDB; AAI80814.
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                                                     (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammation
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                                                                                                                                                                                                                  disorders
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  3, Soppet DR, Olsen HS;
Choi GH, Fiscella M;
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N-PSDB; AAI86846.

The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA019910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides have various cytokine-11ke activities, e.g. stem cell growth factor activity, hematopoisesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or reatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune disorders -Claim 20; SEQ ID NO 20807; 1399pp + Sequence Listing; English. 

0; Gaps Ouery Match 13.0%; Score 55; DB 22; Length 73; Best Local Similarity 44.4%; Pred. No. 26; Matches 12; Conservative 4; Mismatches 11; Indels

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23 LRLGLSDPPASASESTGTTGMSHCSQP 49

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58 LRLGTHGSPTASSQSSATNMAIHRSQP 84

Search completed: March 28, 2003, 09:05:51 Job time: 87.1417 secs

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Gaps

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RECUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE-98049343; PubMed-9389475;

A Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

A Klenk H.-P., Clayton R.J., Gwann M., Hickey E.K., Peterson J.D.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

Richardson D.L., Kerlavage A.R., McKenney K., Adams M.D., Loftus B.,

Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,

Richardson S. N., Meidman J.F., McDonald L., Utterback T.,

Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M.,

Sadow P.W., D'Andrea K.P., Bowman C., Fulii C., Garland S.A.,

Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,

Wenter J.C.,
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reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL: ARONO99; AAB89878.1;
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                                                                                                                                                                                                         Match 21.5%; Score 45.5; DB 5; Length 73; Local Similarity 29.4%; Pred. No. 1.2e+02; les 10; Conservative 7; Mismatches 12; Indels
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Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
NCBI_TaxID=2234;
InterPro; IPR000626; Ubiquitin.
PR0340; ubiquitin; IPR02405; PS50053; UBIQUITIN 2; 1.
SEQUENCE 73 AA; 8738 MM; 61CA839BBA4006A4 CRC64;
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Prof. PP003112; HupF_HypC. 1.
Probom: PD003112; HupF_HypC. 1.
TIGRPAMS; TIGR00074; HypC_hupF; 1.
TIGRPAMS; TORO1097; HUPF_HYPC.; UNKNOWL.1.
Hypothetical protein; Complete protecome.
SEQUENCE 77 AA; 8783 MW; 669179CCB544D027 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hydrogenase expression/formation protein (HYPC)
AF1369
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028902
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                                                  092he6 rickettsia
08tnc3 methanosarc
             Q8umd5 human immun
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Gaps

6

us-09-936-697-5.max.rspt

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-339;
                                                                                                                                                                                                                                                                                                                                  Plasmid pKLH443
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XX MEDINE-21929/06. PubMed-11932238;

X Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Rallen N., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Rallen N., Naylor J., Stenge-Thomann N., Deartelland K., Johnson R.,

Linton L., McEwan P., McKernen R., Talamas J., Tirrell A., Ye W.,

Linton L., McEwan P., McKernen D.E., Grahame D.A., Guss A.M.,

A Limmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Wukhopadhyay B., Reeve J.N., Smith K.,

Rerry J.G., Jarrell R., White R. H., de Macario E.C.,

R Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Mctcalf W.W., Birren B.,

The genome of Methanosarcha acetivorans reveals extensive metabolic

R Cannar Dearty Connar Connar Connar Connar Connar Deartellong Connar Deartellong Connar Connar Connar Deartellong Connar Connar Deartellong Connar Connar Deartellong Connar Connar Deartellong Connar Connar Connar Deartellong Connar Con
                                                                                                                                                                   Smith D.R., Doucette-Steam L.A., Detoughery C., Lee H.-M., Dubois J., Adfacedge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Blartison D., Hoang L., Keagle P., Lumm W., Pothier B., Giu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Juani N., Caruso A., Bush D., Safer H., Parwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Danhels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltah: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 17; Length 60;
Pred. No. 1.5e+02;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 17; Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
NGBLTAXID-2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA; 9082 MW; B6E6AED010FBE62D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6D75EBDB4460C21F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TIEMBLrel. 21, Created)
01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SENSLVAMDFSGQKSRV---IENPTEALSVAVEEGLA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 SEDNIATVDFGGVRQQVKLDLVDDVEEGKYVLVHSGYA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AA.
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9; Mismatches
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ProDom; PD003112; HupF_Hypc; 1.
TIGRFAMs; TIGR00074; hypc_hupF; 1.
                                                                                                                                  STRAIN-DELTA H;
MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000924; AAB86122.1; -. InterPro; IPR001109; HupF_Hypc.
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SEQUENCE 60 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2%;
28.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                        NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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Matches 11;
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Matches
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STRAIN-TAP44-3; TRANSPOSON-TW5044;
MEDLINE-9406912; PubMed-10476039;
Minakhina S., Kholodii G., Mindlin S., Yurieva O., Nikiforov V.;
"TD5053 family transposons are res site hunters sensing plasmidal res sites occupied by cognate resolvases.";
Morobiol. 33:1059-1068(1999).
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Makaryota, Metazoa, Arthropoda, Tracheata, Hexapoda; Insecta,
Pterygota, Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea, Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazel R.G., Chanpe W., Pfeiffer B.D., Wan K.H., Doyle C., Barter E.G., Helt G., Nelson C.R., Miklos G.L.G. Abrill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAINTAP44-3; TRANSPOSON-TN5044;
Kholodii G., Yurieva O., Mindlin S., Gorlenko Z., Rybochkin V.,
Nikiforov V.;
                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "InfoGW4 a novel Tn3 family transposon coding for temperature
sensitive mercury resistance.";
Res. Microbiol. 151:1-12(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Res. Microbiol. 151:1-12(2000).
EMBL: Y17691; CAB65713.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 79 AA: 8626 MW: 1639B3E026E36706 CRC64;
                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MSC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 8.6 kDa_protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                      79 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 MDFSGQKSRVIE-NPTEA-LSVAVEEGLAWRKK 43
12 AMDFSGQKSRVIENPTEALSVAVEEGLA 39
                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                       Xanthomonas campestris.
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borstein P.,
Burtis K.C., Busam D.A., Buller H., Gadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charles B., Doubler A., Deng Z., Mays A.D., Dew I., Diletz S.M.,
RA Borbin K.J., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Barris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houvey B.C., Dunn P.,
RA Harris M.L., Harvey D., Heiman T.J., Hernandez J.R., Houver C.
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alalin M., Mattel B., McIntosh T.C., McHeod M.P., McPherson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Moried M.P., Micherson D.,
RA Nelson R.A., Nixon K., Nuron K., Nuron Y., Nuron K., Nuron K., Nuron K., Nuron K., Nuron K., Sunders R.D.C., Scheeler F., Shen H.,
RA Nelson D.R., Nathon S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue R., Woodage T., Worley K.C., Nu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.W., Rubin G.M., Venter J.C.;
RA Zheng X.H., Zhong F.W., Rubin G.M., Venter J.C.;
C. Ishang X.H., Zhong F.W., Rubin G.M., Venter J.C.;
C. Ishang X.H., Zhong F.W., Rubin G.M., Venter J.C.;
C. Ishang R.R., Werse E.W., Rubin G.M., Venter J.C.;
C. Ishang R.R., Werse E.W., Rubin G.M., Venter J.C.;
C. Ishang R.R., Shang R.M., Zhong W. Zhou X., Zhu X., Smith H.O.,
C. Ishang R.R., Shang R.M., Zhong W. Zhou X., Zhu X., Smith H.O.,
C. Ishang R.R., Shang R.M., Rubin G.M., Venter J.C.;
C. Ishang R.M., Shang R.M., Shang R.S., Shang R
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MEDLINE-20146732; PubMed-10682151;
Masqueller B., Descamps D., Carriere I., Ferchal F., Collin G.,
Masycalles M., Ruffault A., Chanzy B., Izopet J.,
Buffet-Janvresse C., Schmitt M.P., Race E., Fleury H.J.A.,
Aboulker J.P., Yeni P., Brun-Vezinet F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB 5; Length 82;
Pred. No. 2.2e+02;
7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00478; LIM_DOMAIN_1; 1.
PROSITE; PS5003; LIM_DOMAIN_2; 1.
LIM domain; Metal-binding; Zinc.
SEQUENCE 82 Aa; 9207 MW; 94AB7BEFF7150AD7 CRC64;
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NCBI_TaxID=12721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ISENSLVAMDFSGQ----KSRVIENPTEALSVAVEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 ITENAIVALDAKWHRECFKCKKCKTPITASSFVVED 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AA.
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FlyBase; FBgn0030781; CG9644.
InterPro; IFN001781; LIM.
Pfam; PF00412; LIM; 2.
ProDom; PD000094; LIM; 1.
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ilarity 33.3%;
Conservative
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ses 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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209WMQ6
10 09WMQ6
ND 009WM
DT 01-NN
DT 
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Charle R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
Charle R., Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lenz C., Liu A., Liu A., Liu B., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (Jul.-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AC074299; AAR89109 1: --
SEQUENCE 88 AA: 10232 MW; B24F705FE242C581 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kim C., Alonso J., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conney A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukhersky N., Muyyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thaveri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
Theologis A., Ecker J.R.;
"Telomere associated sequence for Arabidopsis thaliana TELIS from
                                                                                                                                                                                                                                                                                                                                                                                                                         3,
"Resensitization and dual HIV-1 resistance to zidovudine and funivodine in the Delta lamivudine roll-over study."; Antivir. Ther. 4:69-77(1999).
EMBL; AJ239270; CRES1518.1; InterPro: TRR00477; RVTSe.
Pfan: PF00078; rvt: 1.
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                                                                                                                                                                                                                                                                                                                                                              Score 43.5; DB 15; Length 69;
Pred. No. 2.1e+02;
8; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                           SEQUENCE 69 AA; 8089 MW; 5BD8FF800A16A70C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
TELIS.2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 LEKEGKISKIGPENPYNTPVFAIKKKEGTKWRK 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                      20.5%;
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nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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es 11; Conserv
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                                                                                                                                                                                                                                                                    69
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Best Local S
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Q9LM11;
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Q9LM1
10 09LM
10 09LM
10 00LO
DT 01-00
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Query Match
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                                                                                                Choanephora infundibulifera.
Eukaryota: Fungl: Zygomycota: Zygomycetes: Mucorales: Choanephoraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M., Alvarenga R., Alvae L.M.C., Araya J.E., Balad G.S., Baptista C.S., Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S., Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H., Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa Reto C.M., Coutlino L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H., Facincani A.P., Ferreira V.C.A., Ferro J.A.,
                                                                                                                                                                                                                                                  Papp T., Vastag M., Acs K., Vagvolgyi C.; "Phylogenetic relationships among Mucoraceae, Choanephoraceae and Glibbertellaceae based on rDNA and glyceraldehyde-3-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                  ä;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                             Score 42.5; DB 3; Length 80;
Pred. No. 3.4e+02;
6; Mismatches 3; Indels
                                                                                                                                                                         Tamms r.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
                                      01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-010-2002 (TrEMBLrel. 21, Last annotation update)
01-010-2002 (TrEMBLrel. 21, Last annotation update)
01-000-2002 (EC 1.2.1.12)
                                                                                                                                                                                                                                                                                                                                                                        80 AA; 8504 MW; 4ECCBEAE035943D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MRT-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein Xf0694.
                       80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 AA.
                                                                                                                                                                                                                                                                                                           EMBL; AJ278315; CACC5562.1; -
Interpro; IPR000173; GAP_dhdrogenase.
Pfam: PF02800; gpdh.C; 1.
Glycolysis; NAD; Oxidoreductase.
                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1 PMRSI---SENSLVAMDFSGQ 18
                                                                                                                                                                                                                                                                                                                                                                                                                                              37 PMKGILGYTENAVVSTDFIGE 57
                                                                                                                                                                                                                                                                                                                                                                                            20.08;
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 9; Conserv
                                                                                                                      Choanephora.
NCBI_TaxID=127959;
                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xylella fastidiosa
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                                                                                                                                                             STRAIN-NRRL 2560;
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                                                                               (Fragment).
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                    09HGR8
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Q9HGR8
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RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
Gardman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kltajima J.P.,
R. Krieger J.E., Kuramee E.E., Laigreet F., Lambais M.R., Leitel L.C.C.,
R.A Lemos B.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
Machado M.A., Mascine E.C., Miyaki C.Y., Monterior Vitorello C.B.,
Mond D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
R.A Mond D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
de Oliveira M.C., de Oliveira H.R., Jr., Pesquero J.B.,
R.A Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Sawasaki H.E.,
A da Silva A.C.R., da Silva A.M., da Silva R.R., Silva W.A. Jr.,
de Sa Z. Jr., Silvaetri M.L., Sakasaki H.E.,
A da Silvaetra J.F., Silvaetri M.L., Silva W.A., de Souza A.P.,
The genome sequence of the plant pathogen Xylella fastidiosa.",
R.M. The genome sequence of the plant pathogen Xylella fastidiosa.",
R.M. Hypothetical protein; Complete protecome.
SEQUENCE 53 AA; 5958 MW; 4B14AF832900832B CRC64;
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MEDLINE-98371265; PubMed-9705261;
MEDLINE-98371265; PubMed-9705261;
Portelli R., Dodd I.B., Xue Q., Egan J.B.;
"The late-expressed region of the temperate coliphage 186 genome.";
Virology 248:117-1301998).
EMBL: U32222; AAC34169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae; P2-like Viruses.
NCBI_TaxID=29252;
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Pred. No. 2.7e+02;
6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 AA; 6491 MW; 1199113D8CDEB8E6 CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 PSELYSLSLTELITWREK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 66.7 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Chlamydia pneumoniae (Chlamydophila pneumoniae). 'Bacteria, Chlamydiales; Chlamydiaceae; Chlamydophila NGB_TAXID=8356;
                                                                                 0928X5 PRELIMINARY; PRT; 79 AA.
0928X5:
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein CPn0209.
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=CWL029;
MEDLINE=99206606; PubMed=10192388;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Q928X5
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                                                                                                                                                                                                                        Avian infectious bronchitis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBI_TaxID=11120;
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NCBL_TAXID=11120;
                                                                                                                                                                                                                                                                                                                                                                                        WEDLINE—57049060; PubMed=8893790;
Wang C.H., Tsai C.T.;
"Genetic grouping for the isolates of avian infectious bronchitis
virus in Taiwan."; for the isolates of avian infectious bronchitis
Arch. VIrol. 141:1677-1688(1996).
BENBL, U38678; AARA136.1; -..
InterPro: IRR002551; Corona_S1.
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"Genetic grouping for the isolates of avian infectious bronchitis
virus in Taiwan.";
Arch. Virol. 141.1677-1688(1996).
EMBL: U38681; AAB47439.1;
Interpro; IPR002551; Corona_S1.
Pfam: PF01600; Corona_S1: 1.
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19.8%; Score 42; DB 12; Length 76; Best Local Similarity 36.4%; Pred. No. 3.76+02.

Matches 8; Conservative 5; Mismatches 9; Indels Matches 9; Indels
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01-NOV-1996 (TrEWBLrel. 01, Last sequence update)
01-JUN-2001 (TrEWBLrel. 17, Last annotation update)
                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                           76 AA.
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                                                                                                                                                                        Spike protein (Fragment).
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SEQUENCE
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Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
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19.8%; Score 42; DB 16; Length 79;
Best Local Similarity 33.3%; Pred. No. 3.9e+02;
Matches 8; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                             19.8%; Score 42; DB 16; Length 79; 33.3%; Pred. No. 3.9e+02; tive 7; Mismatches 9; Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Hypothetical protein CPJ0209.
CPJ0209.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae: Chlamydophila.
                                                               Nat. Genet. 21:385-389(1999).

MEBL; AE001607; AAD18362.1; -
Hypotheitcal protein; Complete proteome.

SEQUENCE 79 AA; 9196 MW; 2813A36311D4A49A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               79 AA
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01-OCT-2000 (TrEMBLrel. 15, Created)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Plant Mol. 18:793-797(1992).
EMBL; M80555; AAK38750.1; -.
HSSP; P37821; 1B8G.
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MEDLINE-92216056; PubMed-1558953;
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Matches 11; Conserv
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                                      HVB12D OR B12DG1.
                                                                                                              NCBI_TaxID=4513;
                          B12D mRNA
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SEQUENCE
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                                                                                                                                               MEDLINE-20150255; Pubwed-10684935; Meder C., Gill S.R., Heidelberg J.F., Sead T.D., Arucham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Galnn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tinsley C.R., Nassif X.;
"Analysis of the genetic differences between Neisseria meningitidis .
"Analysis of the genetic differences between Neisseria expressing two different pathogenicities.";
Proc. Natl. Aced. Sci. U.S.A. 93:11109-11114(1996).

EMBL; U56765; AAC44469:1. -.
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Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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Nucleic Acids Res. 28:1397-1406(2000)
FEMEL: AE002214: AAF38377.1;
TIGR: CP0557;
Hypothedical protein.
SEQUENCE 81 AA: 9455 MM; C6A64877747
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                                                        Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBL_TaxID=83558;
01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2001 (TrEMBLrel. 18, Last annotation update) Hypothetical protein CP0557.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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SEQUENCE FROM N.A.
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Q40019
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STRAIN=CV BOMI;
MEDIARE-94236135, PubMed-8180622;
AAlen R.B., Opsahl-Ferstad H.G., Linnestad C., Olsen O.A.;
"Transcripts encoding an oleosin and a dormancy-related protein are present in both the aleurone layer and the embryo of developing barley (Hordeum vulgare L.) seeds.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
Hordeum vulgare (Barley).
Kakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticaea; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steinum T.M., Berner H., Stacy R.A.P., Salehlan Z., Aalen R.B.;
Differential regulation of the barley (Hordeum vulgare) transcripts
B22E and B12D in mature aleurone layers.";
Physiol. Plantarum 102:337-345(1998).
EMBL; X706604; CAA74065.1;
EMBL; X708005; CAA70936.1;
SEQUENCE 87 AA; 9648 MW; EECE117231E51046 CRC64;
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"Identification and characterization of three putative genes for 1-
aminocyclopropane-1-carboxylate synthase from etiolated mung bean
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01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-UNV-1901 (TREMBLrel. 17, Last annotation update)
1-aminocyclopropane 1-carboxylate synthase (Fragment).
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69 AA; 8057 MW; EAD4BDE77D47735D CRC64;
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tive 7; Mismatches 16;
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Pred. No. 4.6e+02;
9; Mismatches 14
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EDUDENCE FROM N.A.

SEQUENCE FROM N.A.

RATCC 3595 / DSM 2834;

RECTRAIN-CZA / ATCC 3595 / DSM 2834;

REDINE-21929760; Pubbwed-1192238;

Ralagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RICHIGHA W., Calvo S., Rhoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArcllano K., Johnson R.,

Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Lincon L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Ladderich R., Indram-Smith C., Kuettner H.C., Krzycki J.A.,

Springer T.A., Umayam L.A., White R.H., de Macario E.C.,

Rery J.G., Jarrell K.F., Jing H., Macario A.J.L., Panlsen I.,

Retcalf W.W., Birren B.;

Ratcalf W.W., Birren B.;

R. The genome of Methanosarcina acetivorans reveals extensive metabolic
                                                                                     Thermoanaerobacter tengcongensis.
advertal, Flimicutes; Bacillus/Clostridium group; Clostridia;
Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
NCBL_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                19.3%; Score 41; DB 16; Length 85; 30.0%; Pred. No. 5.8e+02; tive 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%: Score 41; DB 17; Length 87; illarity 22.7%; Pred. No. 6e+02; Conservative 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanosarcina acetivorans.
Archaea: Euryarchaeota; Methanoscoci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
NCBI_Tax.D=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AA; 10125 MW; 1A970190E4B5CD2D CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AA
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Genome Res. 12:532-542(2002).
EMBL; AE011028; AAM06620.1; -.
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Best Local Similarity 30.v.
Best ... 9; Conservative
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Best Local Similarity
Matches 10; Conserv
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  TTE1677
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Q74620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                  Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xanthomonas campestris (pv. vesicatoria).
Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
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SEQUENCE FROM N.A.
GLOW, Han Z., Fu G., Chen Z.;
GNOUNCE Genes expressed in human dentritic cell.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201935; AAF86871.1;
SEQUENCE 79 AA; 9460 MW; 783381BD6DAFB7AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.3%; Score 41; DB 2; Length 85; 44.4%; Pred. No. 5.8e+02; tive 4; Mismatches 6; Indels
                                                                     01-027-2000 (TrEMBLrel. 15, Created)
01-027-2000 (TrEMBLrel. 15, Last sequence update)
01-027-2000 (TrEMBLrel. 15, Last annotation update)
021-027-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TERMILAEL: 12, Created)
01-NOV-1999 (TERMILAEL: 12, Last sequence update)
01-NOV-1999 (TERMILAEL: 12, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein TrEl677.
                                                  79 AA.
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Matches 10; Conservative
                                              PRELIMINARY;
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es 8; Conservative
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                                                O9NRP2
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              RESULT 20
Q9NRP2
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1D 06
AC 06
DT 01
DT 01
DE DT 01
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us-09-936-697-5.max.rspt

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Quinones-Wateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
"Point mutant frequencies in the pol gene of human immunodeficiency
virus type I are two to threefold lower than those of env.";
AIDS Res. Hum. Retroviruses 12:1117-1128(1996).
BEMBL, U14846; AAC55733.1;
InterPro; IPR00477; RVTSe.
Ffam: PF00078; TVt; I.
FRNA-directed DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDITARE-97000986; Pubmed-8844016;
Quinones-Mateu M.E., Holguin A., Dopazo J., Najera I., Domingo E.;
"Point mutant frequencies in the pol gene of human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40.5; DB 15; Length 68; Pred. No. 5.2e+02; 7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 68 68 68 SEQUENCE 68 AA; 7910 MW; 187F11C0FCE674C8 CRC64;
                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Reverse transcriptase (Fragment).
                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retrold viruses; Retroviridae; Lentivirus.
NCBL:TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Reverse transcriptase (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 MDFSGQKSRV-IENP--TEALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.1%;
ilarity 33.3%;
Conservative
                                                                                                                                                                                                                                                                                  g therapy.";
Virol. 69:23-31(1995).
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J. Virol. 69:23-31(1995).
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PRELIMINARY;
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es 11; Conserv
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SEQUENCE FROM N.A.
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Gaps
virus type 1 are two- to threefold lower than those of env.";
EMBL; U14856; AAG55763.1;
InterPro; IPR000477; RVTse.
Flam; PF00078; rVt. 1.
FNA-directed DA Polymerase.
NON TER 18 68 68
SEQUENCE 68 AA; 7938 MW; 18678049FCE674C8 CRC64;
                                                                                                                                                                                   Query Match
19.1%; Score 40.5; DB 15; Length 68;
Best Local Similarity 33.3%; Pred. No. 5.28+02;
Matches 11; Conservative 7; Mismatches 12; Indels 3
                                                                                                                               68 AA; 7938 MW; 18678049FCE674C8 CRC64;
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5.1.4_p5_4578 Compugen Ltd.	Search time 9.48032 Seconds	0.123 MIIIION CEII UPGATES/SEC			ters: 7863		results predicted by chance to have a to the score of the result being printed, of the total score distribution.		Description	Q60262 methanococc Q57649 methanococc Q57987 methanococc	P31337 staphylococ P28690 escherichia P39243 bacteriopha	P48859 streptomyce P52336 nostoc sp. P29827 streptovert	P00202 methanosarc P10604 desulfoylbr	Control transfer of the Control of t	. 005302 mycobacteri Q927r1 chlamydia p 084529 chlamydia t	028560 archaeoglob Q01761 streptomyce O9v249 homo sanien	mus m	P41072 escherichia P50154 bos taurus P16001 paramecium	P22755 bacillus 1i P48784 methanobact P01051 hirudo medi	O9uh64 homo sapien PO\$24 human immun O64254 mycobacteri	P48783 methanobact P50483 methanobact
GenCore version Copyright (c) 1993 - 2003	OM protein - protein search, using sw model Run on: March 28, 2003, 08:56:00 ; Se	Therefore: US-09-936-697-5	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	hed: 112892 seqs	Total number of hits satisfying chosen parameters Minimum DB seq length: 40 Maximum DB seq length: 90	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 1000 summaries Listing first 1000 summaries Listing first 2000 summaries	No. is the number of greater than or equal s derived by analysis	8 Ouery	Score Match Length DB	1 46.5 21.9 62 1 YZO5_METJA 2 46 21.7 73 1 RPON_METJA 3 42 19.8 82 1 Y567_METJA	40 18.9 82 1 39 18.4 45 1 39 18.4 71 1	38.5 18.2 67 1 38.5 18.2 74 1 38.5 18.2 78 1	38 17.9 59 1 38 17.9 63 1 38 17 9 72 1	38 17.9 72 1	36.5 17.2 88 1 36.5 17.2 88 1	36 17.0 59 1 36 17.0 66 1 36 17.0 76 1	36 17.0 76 1 36 17.0 80 1	35.5 16.7 69 1 35.5 16.7 75 1	35 16.5 58 1 35 16.5 67 1 35 16.5 70 1	35 16.5 79 1 34.5 16.3 80 1 34 16.0 51 1	34 16.0 67 1 34 16.0 67 1

bacteriopha escheriopha escherichia acalolepta escherichia archaeoglob variola vir archaeoglob variola vir archaeoglob bungtra pu porphyra pu avian infec escherichia avian infec carica cand pungtra aco mycoplasma carica cand avian infec escherichia purchoplusi carica cand pungtra aco mycoplasma escherichia escherichia escherichia porrella bu archaeoglob human immun avian infec avi

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P51713 bacteriopha P58726 aslmonella P30818 salmonella P07076 bacteriopha P03086 polyomaviru P22151 neurospora P07593 yersinia en	mycoplasm mycobacte escherich haemophil	aquif synec human autog	049310 mycophasma 049310 mycophasma 099943 streptococc 008366 arabidopsis P14572 cenothera b P05717 pisum sariv	P13547 trittcum ae Q24152 drosophila P33911 bacillus su Q9xyzl conus pulic Q95mn neisseria m	V0220 g1VLINE max 09ppn8 ureaplasma P49267 aptostichus P4730 rattus norv P23689 human adeno P10512 escherichia P05836 escherichia		090111 pasteurella 090111 pasteurella 09zmbb helicobacte P44260 haemophilus P31330 desulfovibr P07470 bos taurus P06353 hordeum vul P27372 synechocyst	P79189 quillardia P7654 escherichia Q0eyfi escherichia 000107 pavlova lut P11221 pseudomonas P57670 thermoplasm P62595 haliotis la P00111 porphyra te	
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P12151 Onyza sativ Q92gd& rickettsia Q97115 sulfolobus Q97306 aeropyrum p P54009 methanococc P27193 escherichia Q96033 homo sapten	09z224 mus musculu 069z50 bacillus me P75131 mycoplasma 09uhp9 homo sapien 097cul thermoplasm	P02346 bacillus st 091a09 dicentrarch P51185 klebsiella P82708 bos taurus P51421 zea mays (m	P12170 marchantia P1697 staphylococ Q9r5h8 dactylococc P15762 sinapis alb P44045 haemophilus P52136 escherichia	P16350 vicia sativ P21899 trypanosoma P14795 trypanosoma P02868 vicia cracc 029364 archaeoglob P33710 canis famil	P05579 circus aeru P05579 circus aeru P05563 spheniscus P20846 vultur gryp 095650 homo sapien P03769 bacteriopha	083262 treponema p P04542 canis famil P01124 homo sapien 006718 bacillus su 048425 bacteriopha Q38666 bacteriopha P21305 methanococc P21305 saccharomoc		P80250 Fattus norv Q9C114 lactococcus Q9exd7 mycoplasma P88085 earopyrum p P29199 haloarcula Q9yfg3 aeropyrum p R38592 halichoerus Q9y811 pyrococcus Q9y812 pyrococcus	028690 archaeoglob 028690 archaeoglob 00929 caenorhabdi 14147 perameles g P19873 cucurbita m P3856 clostridium 09v1u2 pyrococcus 074094 pyrococcus 075888 arcorhizoblu 09rh31 ancylobacte P41651 pinus thunb 08739 treponema p P74641 synechocyst
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P49197 caenorhabdi O10355 orgyia pseu O9fft8 phaseolus a P33134 salmonella P642015 heterodontu O9408 chlamydia m O84088 chlamydia m O84088 chlamydia m O84088 chlamydia m O8408 chlamydia m O8408 chlamydia m O8408 chlamydia m O8408 chlamydia m O8408 chlamydia m O85275 rhizoblum m O87275 rhizoblum m O87297 mothorolasm O87297 mothorolasm O87297 methanopyru O97778 methanopyru O97778 methanopyru O9778 methanopyru O9778 methanopyru O9778 methanopyru O9778 methanopyru O97806 mycobacteri O10189 schlacsacch D7621 scherichia O8506 mycobacteri O8506 mycobacteri O8506 mycobacteri O8506 mycobacteri O8506 mycobacteri O8506 methanopyru O8506 ceretitis ch O8507 phrococcus O8501 methanother O8501 methanother O8902 phrococcus O8902 phrococcus O8902 phrococcus O8902 prococcus O8902 prococcus O8902 prococcus O8902 methanother O8902 methanother O8902 methanococc O8902	Q44156 actinobacil Q9wxi8 buchnera ap Q9pr18 qallus gall P45596 streptococc O83440 treponema p Q9wxk8 streptococc
88   RSZ1_CAEEL 88   1 VOOZ_NPVOP 89   1 ALB1_PHAAU 89   1 FLIO_SALIY 89   1 FLIO_SALIY 89   1 FLIO_SALIY 89   1 RL28_CCHLNU 89   1 RL28_CCHLNU 89   1 RL28_CCHLNU 89   1 RL28_CCHLNU 89   1 VRNB_MYCCA 90   1 AX6E_SOYEN 91   1 AREA_BESTOY 91   1 AREA_BESTOY 92   1 AX6E_SOYEN 93   1 AX6E_SOYEN 94   1 AX6E_SOYEN 95   1 AX6E_SOYEN 96   1 AX6E_BESTON 96   1 AX6E_BESTON 97   1 AX6E_SOYEN 98   1 AX6E_BESTON 98	84 1 85 1 86 1 86 1 87 1
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                    bradyrhizob
blaberus di
rhizobium m
synechocyst
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bacteriopha
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        vaccinia vi
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BUELINE-96337999; bubhed-8688087;

Bult C.J. White O. Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.C., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Strainage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Retch C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen NS.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
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0017128
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083277
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1009x139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus. NCBL_TaxID=2190;
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SEQUENCE 62 AA; 7327 MW; 1624EC72E75EBAD7 CRC64;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJECLO5.
                                                                                                                                                                                                                                                                                                                                                                      62 AA
                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Complete proteome. DOMAIN 3
                                                                           YD21_THEMA
GP60_BPSP1
UL11_HSV7J
                                                IF1_RHIME
Y738_SYNY3
                                                                                                                                   SECE_METJA
GVA1_HALN1
                                                                                                                                                                HPIS_RHOFE
                                                                                                                                                                                           TALA CARMA
                                                                                                                                                                                                          7250_TREPA
                                                                                                                                                                             RL28_BUCAI
                                                                                                                                                                                                                      CC68_PINTH
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L77118; AAC37071.1; -. TIGR; MJECL05; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    YZ05_METJA
Q60262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٦,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      jannäschii.";
Science 273:1058-1073(1996),
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                              Stateon G.C., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Stateon G.C., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D., Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I., Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Gtochaek R., Kalkness E.F., Weinstock K.G., Merrick J.M., Glodek A., Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10 RNA POLYMERASE SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01112; RNA_POL_N. 1.
PROSITE; PS01112; RNA_POL_N_BKD; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Metal-binding; Complete proteome.
METAL
7 ZINC (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                         Methanococcus jannaschii.
Archaea: Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
E716EA406D65B831 CRC64;
            RPON_METJA STANDARD; PRT; 73 AA. 057649; 01-NOV-1997 (Rel. 35, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) DNA-directed RNA polymerase subunit N (EC 2.7.7.6). RPON OR MJ0196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 20; 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 PMRSISENSLVAMDFSGQKSRVI - - ENPTEAL 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46;
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE-96337999; Pubmed-8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR000268; RNA_PO1_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67475; AAB98176.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AA; 8695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                              NCBI_TaxID=2190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA)(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y567_METJA
ID Y567_METJA
AC Q57987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
RPON_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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increases during stationary phase.";
J. Bacteriol. 183:2765-2773(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=K12;
MEDLINE=90337272; PubMed=2199308;
                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequ
16-OCT-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                        15 FSGQKSRVIENPTEALSVAVEE 36
                                                                                                                                                   EMBL; K02985; AAA26680.1; -. InterPro; IPR001405; Radc.
                                                                                                                                                                                                                                                                                     18.9%;
40.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence
Science 277:1453-1474(1997).
                                                                                                                                                                                      ProDom; PD007415; RadC; 1.
PROSITE; PS01302; RADC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli, and
                                                                                                                                                                                                                                                                                                   Local Similarity
es 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                        DNA repair.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RS22_ECOLI
P28690;
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RS22_ECOLI
                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                           QQ
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                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-9633799; PubMed-868887;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

COLTON M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borddowsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murphy E., Loefdahl S.;
"Transposition of Th554 does not generate a target duplication.";
Nature 307:292-294(1984).
-i. FUNCTION: INVOLYED IN DNA REPAIR (BY SIMILARITY).
-i. SIMILARITY: BELONGS TO THE RADC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA repair protein radC homolog (25 KDa protein) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 1; Length 82;
Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JAN-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                   Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 protein; Complete proteome.
82 AA; 8766 MW; 3F3810EEFC9F81CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LVAMDFS-GQKSRVIEN-----PTEALSVAVEEGLAWR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28 LVSMGINIGSKLKVIRNQNGPVIISTKGSNIAIGRGLAMK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firmicutes; Bacillales; Staphylococcus
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MJ0567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=84117462; PubMed=6320000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U67505; AAB98558.1; -. TIGR; MJ0567; -.
                                                                                                                                                                                                                                                                                                                                                                                       Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.8%;
ilarity 32.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A.
                                                                                      Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=2190;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local S...
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RADC_STAAU
P31337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RADC_STAAU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
STRAIN-K12 / MG1655;
MEDLIN-K12 / PUNMED -9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahajan S.K., Chu C.C., Willis D.K., Templin A., Clark A.J.; "Physical analysis of spontaneous and mutagen induced mutants of Escherichia coli K.12 expressing DNA exonuclease VIII activity."; Genetics 125:261-273(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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0
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STARAL-KLZ / WA3110;
MEDLINE-21189300; Pubmed-11292794;
Izutsu K., Wada C., Komine Y., Sako T., Ueguchi C., Nakura S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-0157.H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; Pubmed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
30S ribosomal protein S22 (Stationary-phase-induced ribosome-associated protein) (SRA) (Protein D).
PREV OR SAR OR B1480 OR 22230 OR ECS2084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1; Length 82;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 AA; 8920 MW; 65E8BF06E3DEC3A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 AA.
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Page 10

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HSSP; P32081; 1CSP.
InterPro; IPR002059; Cold_shock.
Pfam; PF00313; CSD; 1.
                                                                                                                                                                                                                                                                         EMBL; AF158101; AAD42616.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL132662; CAB59584.1; -.
                                                                                                                                                                                                                                                                                                                                                                              18.4%;
illarity 32.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X92686; CAA63367.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P32081; 1CSP
                                                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSPF_STRCO
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CSPF_STRCO
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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ROSE D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blatther F.R.; Grome sequence of enterohaemorrhagic Escherichia coll 0157:H7.", Nature 409:529-533(2001).
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T4-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoncation update)
Hypothetical 8.1 kDa protein in ndd-denB intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 45; Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81DB6E2D2E22C2F CRC64;
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EMBL; AEDO0245; ARC74553.1;
EMBL; AEDO5357; AAG5689.1;
EMBL; AP002557; BABN34677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D13179; BAA02474.1; -.
EMBL; X55956: -: NOT ANNOTAT
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DNA Res. 8:11-22(2001).
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ID Y16K_
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STRAIN-A.3(2) / M145;
STRAIN-A.3(2) / M145;
STRAIN-A.3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Hung C.-H., Kleser T., Larke L., Murphy L., Ollyer K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cold shock protein soci
SCOF ON SCOOS AS SCORISTON SCRII.07C.
Streptomyces coelicolor.
Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae, Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBL TaxID-1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coelicolor A3(2).";

substant A17(2002).
-!- SUBGELJULAR LOCATION: Cytoplasmic (Potential).
-!- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
-!- INDUCTION: IN RESPONSE TO THE COLD-SHOCK DOMAIN (CSD) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Av-Gay Y., Ravin S., Aharonowitz Y., Cohen G.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                               ll protein.
71 AA; 8143 MW; 5D56546D2FADAFOC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 1; 1
Pred. No. 1.6e+02;
5; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 PLKSTSEKMTVNATLANNSNERFCIENDTETYTV 59
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MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-9708667; PubMed-8932316;
MEDLINE-9708667; PubMed-8932316;
MEDLINE-9708667; PubMed-8932316;
METAL D.R., Bedbin T.J., Thorsteinson M.V., Bassam D., Brass S.,
Ernst A., Bogger P., Pearl H., Mulligan M.E., Potts M.;
Mill D.R., Bogger P., Pearl H., Mulligan M.E., Potts M.;
Gland (cyanoglobin) is a peripheral membrane protein that is
restricted to certain Nostco spp.";
J. Bacteriol. 178:6587-6598(1996).
I- FUNCTION: THE KEY ENZYMATIC REACTIONS IN NITROGEN FIXATION ARE
CATALYZED BY THE NITROGENASE COMPLEX, WHICH HAS 2 COMPONENTS: THE
IRON PROTEIN AND THE MOLYBDENUM-IRON PROTEIN.
CATALYTIC ACTIVITY: 8 reduced ferredoxin + 8 H(+) + N(2) + 16 APP
8 OXIDIZED GEREFOXIN + 2 NH(3) + 16 ADP + 16 phosphate.
I- COFACTOR: BINDS ONE 4PE-4 CLUSTER PER DIMER.
I- SUBUNIT: HOMODIMER (BY SIMILARITY).

1- SIMILARITY: BELONGS TO THE NIFH / BCHL / CHLL FAMILY.
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PRINTS; PR00050; COLDSHOCK.
ProDom: PD000621; Cold_shock: 1.
SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK: 1.
Transcription regulation; DNA-binding; Activator; Complete proteome.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                prostre; PF00142; fer4_NifH; I. PARTIAL. PROSTRE; PS00546; NIFH_FRXC_1; PARTIAL. PROSTRE; PS00746; NIFH_FRXC_1; PARTIAL. Oxidoreductase; Nitrogen firation; Iron-sulfur; 4Fe-4S; ATP-binding. NP BIND 13 20 ATP (POFENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nitrogenase iron protein (EC 1.18.6.1) (Nitrogenase component II)
(Nitrogenase Fe protein) (Nitrogenase reductase) (Fragment).
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Pred. No. 2e+02;
7; Mismatches 13; Indels 1
                                                                                                                                                               18.2%; Score 38.5; DB 1; Length 67; 39.3%; Pred. No. 1.8e+02; ive 2; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nostoc sp. (strain MUN 8820).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 SENSLVAMDFSGQKSRVI------ENPTEALSVAVEEG 37
                                                                                                        DOMAIN 4 64 CSD.
SEQUENCE 67 AA; 7179 MW; E4FDAD9BB1D92B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 AA; 7919 MW; 14B88F560242DCDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    74 AA.
                                                                                                                                                                                                                                            3 RSISENSLVAMDFS-GQKSRVIENPTEA 29
                                                                                                                                                                                                                                                                                  40 RELOEGOAVTFDITOGOKGPOAENITPA 67
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25.5%;
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                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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es 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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SEQUENCE
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Matches
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23 SONTLAAMAEMGORILIVGCDPKADSTRLMLHSKAQTTVLHLAAERG 69

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SEQUENCE OF 60-78.

AN EDLINE-8929158; PubMed-224454;

Naruse N., Tenmyo O., Tomita K., Konishi M., Miyaki T., Kawaguchi H.,
Naruse N., Tenmyo O., Tomita K., Konishi M., Miyaki T., Kawaguchi H.,
Naruse K., Wakamiya T., Shiba T.,
Lanthiopeptin, a new peptide antiblotic. Production, isolation and
Properties of lanthiopeptin, ";
J. Antiblot. 42:837-845(1989).
C. THE ANIOTENSIN-CONVERTING ENZYME PHOSPHOLIPASE A2, AND
OF THE ANIOTENSIN-CONVERTING ENZYME. SHOWS INHIBITORY ACTIVITIES
C. THE ANIOTENSIAL ACTIVITIES AND IMMUNOPOTENTAATING ACTIVITIES
C. THE SEY, AND CYS INTO DEHVORATED AA AND THE FORMATION OF SULFIDE
C. THE SEY, AND CYS INTO DEHVORATED AA AND THE FORMATION OF SULFIDE
CLEAVAGE OF THE MODIFIED PRECURSOR.
CLEAVAGE OF THE MODIFIED PRECURSOR.
C. SIMILARITY: STRUCTURAL SIMILARITY TO OTHER TYPE B LANTIBIOTICS.
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                                                                                                                                                                                                                                                                                        STRAIN-MAR 164C-MY6;

BEDLINE-3101152; PubMed=2070795;

Kaletta C., Bridan K.-D., Jung G.;

Ratecta C., Bridan K.-D., Jung G.;

"Prepeptide sequence of cinnamycin (Ro 09-0198): the first structural

"Prepeptide sequence of lantibloctic.";

Eur. J. Biochem. 199:411-415(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91107436; PubMed=2125590; Fredenhagen A., Fendrich G., Marki F., Marki W., Gruner J., Racdenhagen A., Fendrich G., Marki F., Marki B., Gruner J., Baschdorf F., Peter H.H.; "Duramycins B and C, two new lanthionine containing antibiotics as inhibitors of phospholipase A2. Structural revision of duramycin and
                                                                                                                                                   Streptoverticillium griseoverticillatum.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=68215;
                                                            01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Lantibiotic cinnamycin precursor (Lanchiopeptin) (Lantibiotic RO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYSINOALANINE (BONDED TO 65).
ALS-S-CYS (LANTHOININE).
ABH-S-CYS (BETA-METHYLLANTHIONINE).
ALA-S-CYS (BETA-METHYLLANTHIONINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D-ABU (AMINOBUTYRIC ACID).
D-ABU (AMINOBUTYRIC ACID).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANTIBIOTIC CINNAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibiotic; Bacteriocin; Lantibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibiot. 43:1403-1412(1990).
                                      (Rel. 25, Created)
(Rel. 25, Last sequ
(Rel. 40, Last anno
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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S17181; EWSMYG.
A45767; EWSMCN.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 60-78.
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
77
77
78
63
64
                                                                                                                                              CINA OR ROCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cinnamycin.";
                                      01-APR-1993
CINA_STRGV
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us-09-936-697-5.max.rsp

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PRT;
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB005550; BAA21477.1; -. PIR; S07154; FEDV2V. HSSP; P00210; 1FXR.
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27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53
7091 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 27.0 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acidophilum.";
Nature 407:508-513(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
14
17
53
63 AA;
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Q9HL09;
           SEOUFINGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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01-JUL-1989 (Rel. 11, Last sequence update)
01-DUC-1998 (Rel. 13, Last annotation update)
Ferredoxin II (Fd II).
Desulfovibrio vulgaris (strain Miyazaki).
Bacterla; Proteobacteria; delta subdivision; Desulfovibrio.
  ABU-S-CYS (BETA-METHYLLANTHIONINE).
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M., Konishi T., Kawanishi K., Ohashi K., Kishida M.,
Kohno K., Akutsu H., Kumagai I., Nakaya T.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                         ilarity 34.2%; Score 38.5; DB 1; Length 78; and No. 2.1e+02; Conservative 6; Mismatches 10; Indels
                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.9%; Score 38; DB 1; Length 59; nlarity 35.7%; Pred. No. 1.8e+02; Conservative 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Methanosarcina barkeri.
Archaea; Euryarchaeote; Methanococci; Methanosarcinales;
Methanosarcinaceae; Methanosarcina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIMITS: PRO0037; fer4; 2.
PRINTS: PRO00353; 4FE4SERDOXIN, 2.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
ELECTRON transport; Iron-sulfur; 3Fe-4S.
SEQUENCE 59 AA; 6121 MW; 22D1EB8E44342CA CRC64;
                                                                                                                                    4 SISENSLVAMDFSGQKSRVIENP-----TEALSVAVE 35
                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                         59 AA.
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                                                                                                                                                                                                                                                                       PRT;
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60 77
78 AA; 8205 MW;
                                                                                                                                                                                                                                                                     STANDARD;
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                                                                             Local Similarity
les 13; Conserva
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es 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  Ferredoxin
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P00202;
                      SEQUENCE
                                                              Duery Match
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THIOETH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-20479972; PubMed-11029001; Methop A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; The genome sequence of the thermoacidophilic scavenger Thermoplasma
MEDLINE-89274328; PubMed-2855025; Okawara N., Ogata M., Yagi T., Makabayashi S., Matsubara H.; Okawara N., Ogata M., Yagi T., Makabayashi S., Matsubara H.; "Characterizatlon and complete amino acid sequence of ferredoxin II from Desulfovibrio vulgaris Miyazaki."; Biochimie 70:1815-1820(1988).
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                                                                                                                                                                                                                 Biochime 70:1815-1820 (1988).
-i- FUNCTION: FERREDOXINS ARE IRON-SULFUR PROTEINS THAT TRANSFER ELECTRONS IN A WIDE VARIETY OF METABOLIC REACTIONS.
-i- COFACTOR: BINDS 1 4FE-4S CLUSTER.
-i- SUBDUNTY: HOMODIMER.
-i- SIBILIARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
IRON-SULFUR (4FE-4S).
82232C1244A5C84B CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR0037; fer4; 1.
PRINTS; PR00352; 3FE4SFRDOXIN.
PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
PROFICE TROSPORT; Tron-sulfur; Repeat; 4Fe-4S.
INIT_MET
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Pred. No. 1.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001080; 3Fe4S_ferredoxin.
InterPro; IPR001450; 4Fe4S_ferredoxin.
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RESULT 15
VG85_BPML5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S., Kawashima T., Amano N., Koike H., Yamazaki M., Kanehori K., Kawamoto T., Kawashima Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Suzuki M.; Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium."; Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).

-I. FUNCTION: DNN-dependent RNA polymerase catalyzes the transcription of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPON / EUKARYOTIC RPB10
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                            .,
                                                                                                                                                                      InterPro; IPR000268; RNA_pol_N.
Pfam; PF01194; RNA_pol_N; 1.
PROSITE; PS01112; RNA_POL_N_8KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                             Length 72;
                                                                                                                                                                                                                                                                                                                                                                          20; Indels
                                                                                                                                                                                                                                                                  ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
792AEDA20E5447E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
DNA-directed RNA polymerase subunit N (EC 2.7.7.6).
                                                                                                                                                                                                                                           ZINC (BY SIMILARITY).
ZINC (BY STMITARITY).
                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1;
Pred. No. 2.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                             4 PVRCFSCGRVIASDYGRYIKRVNEIKAEGRDPSPEE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 AA.
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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MEDLINE-20570466; Pubmed-11121031;
 RNA POLYMERASE SUBUNIT FAMILY
                                                                                                                                                                                                                                    Metal-binding; Complete proteome.
7 7 2 21NC
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                                                                                                                                               EMBL; AL445064; CAC11573.1; -. HSSP; O26147; 1EF4.
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                                                                                                                                                                                                                                                                                                                                            17.9%;
30.6%;
                                                                                                                                                                                                                                                                                            54 54
72 AA; 8368 MW;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermoplasma volcanium.
                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUN-2002
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Q979K0;
                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91358306; PubMed-1885512;
Yen K.-M., Katil M.R., Blatt L.M., Simon M.J., Winter R.B.,
Fausset P.R., Lu H.S., Harcourt A.A., Chen K.R.;
Fausset P.R., Lu H.S., Harcourt A.A., Chen K.R.;
Fuloning and characterization of a Pseudomonas mendocina KRI gene
cluster encoding toluene-4-monooxygenase.";
J. Bacteriol. 173:5315-5327(1991).
I- FUNCTION: HYDROXYLARES TOLORNE TO FORM P-CRESOL.
COFACTOR: FAD; REQUIRES FEC+2) FOR ACTIVITY.
I- SUBMINT: THE MULTCOMPOUND: first Step.
IS SURMED BY THE THOA, THOB, TMOC, TMOD, TMOE AND TMOF
Pfam, PF01194; RNA_pol_N; 1.
PROSITE; PS01112; RNA_POL_N_8KD; 1.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                            Length 72;
                                                                                                                                                                                                                                                                                2.3e+02;
2.3e+02;
20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Toluene-4-monooxygenase system protein B (EC 1.14.13.-).
                                                                                                             ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
ZINC (BY SIMILARITY).
OGAECOAA7AC75CA6 CRC64;
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Pred. No. 2.6e+02;
1; Mismatches 4;
                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                   4 PVRCFSCGRVIASDYGRYLRRINEIRSEGREPTAEE 39
                                                                                                                                                                                                                                                                                                                                                                          1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 AA.
                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
                                                                                                                                                                                                                                                                         Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                     Pred.
                                                                                 Metal-binding; Complete proteome METAL
                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                 SEQUENCE 72 AA; 8483 MW;
                                                                                                                                                                                                                                                                      17.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M65106; AAA26000.1; -
                                                                                                                                                                                                                                                                                               Local Similarity 27.8 es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas mendocina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 NPTEALSVAVEE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 NPTEVIDVVFEE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
ses 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMOB_PSEME
                                                                                                                                                                                                                                                                      Query Match
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Davis R.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-20150255; PubMed=10684935; Med T., Heidelberg J.F., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gynnn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.,
                                                                                                                                                                                               Hatfull G.F., Sarkis G.J.;
DNA sequence, Structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99206606, PubMed-10192388,
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
Olinger L., Grimwood J., Davis R.W., Stephens R.S.,
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
                                                                                                               Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae; L5-11ke viruses.
NCBL_TAXID=31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
130-Leic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 88;
Pred. No. 3.8e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                             EMBL; 218946; CAA79461.1; -.
PIR; S31030; S31030.
SEQUENCE 88 AA; 10159 MW; 2927841F7D6D4ABC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBL:raxID=03558;
                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RS19_CHLPN STANDARD; PRT; 88 AA. 0927R1; 0947R8; 30-MAY-2000 (Rel. 39, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 30S ribosomal protein S19. RPSS OR RS19 OR CPN0643 OR CP0104.
   88 AA.
                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-93211282; Pubmed-8459766;
                                                                                                                                                                                                                                                                                                                                                                                                                                         17.5%; 50.0%;
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 EALSVAVEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EALFDITWDGVAWAKK 76
                                                                     Gene 85 protein (GP85).
                                                                                                 Mycobacteriophage L5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 8; Conserv
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VG85_BPML5
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          SPECIES—C.trachomatis, STRAIN-D/UW-3/Cx;
BEDILNE-9000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-C. muridarum; STRAIN-MOPn / Nigg;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.2%; Score 36.5; DB 1; Length 88; 26.2%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR00,222; Ribosomal_S19.
Pfam; PF00203; Ribosomal_S19; 1.
ProDom; PD001012; Ribosomal_S19; 1.
PROSTIE; PS00323; RIBOSOMAL_S19; 1.
Ribosomal protein; rRNA-binding; Complete proteome.
CONFILCE 88 AA; 10201 MW; EB1E98E3B4BC2588 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 PIKTWSRRSMITPEMIGHTFEV-HNGKKFLTVFVSETMVGHK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydia muridarum.
Nacteria: Chlamydiales; Chlamydiaceae; Chlamydia.
Eds.TaxiD-e813, 83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                        EMBL, AE001647; AAD18782.1; -. EMBL, AE002173; AAF73629.1; -. EMBL, AP002547; BAA98850.1; -. HSSP; PR0381; 10KF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 282:754-759(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 26.2 es 11; Conservative
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CSP7_STRCL
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Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Nucled Acids Res. 28:1397-1406(2000)
Nucled Acids Res. 28:1397-1406(2000)
TOTHE TOTHE TOTHE STRONGEN ACOMPLEX WITH S13 THAT BINDS STRONGEY TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).

1. SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftur B.,
Overbeck R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.W., D'Andrea K.D., Neidman J.F., McDonald L., Utterback T.,
Mason T.W., Olsen G.J., Fraser C.M., Smith H.O., Noese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.2%; Score 36.5; DB 1; Length 88; 26.2%; Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERMITS PRO0203: Ribosomal_S19; T. PRON203: Ribosomal_S19; T. ProDom: PD001012: Ribosomal_S19. TIGRPAMS: TIGROID050: Fabscbact; 1. PROSITE; PS00323; RIBOSOMAL_S19; T. Ribosomal_S10; T. Ribosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1::: | | :: | | : | | 30 PIKTWSRRSMITPEMIGHTFEV-HNGRKFLTVFVSETMVGHK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein AF1713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reducing archaeon Archaeoglobus fulgidus ".
Nature 390:364-370(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
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MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR002222; Ribosomal_S19.
0203; Ribosomal_S19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE001323; AAC68125.1; -. EMBL; AE002347; AAF73605.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P80381; 1QKF.
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028560;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
cold shock-like protein 7.0.
SC7.0.
Streptomyces clavuligerus,
Bacteria, Actinobacteria; Actinobacteria Actinomycetales;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                   4;
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0
                                                                                                                                                                                                                                                                                       17.0%; Score 36; DB 1; Length 59; 31.0%; Pred. No. 3.3e+02; Live 4; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Indels
                                                                                                                                                                                                            11 protein; Complete proteome.
59 AA; 6867 MW; C62D3AlD9DDDFE35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 63 CSD.
66 AA; 7016 MW; CCD5C7858FEB4707 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00357; CSP; 1.
PROSITE; PS00352; COLD_SHOCK; 1.
DOMNIN 4 63 CSD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-40.
STRAIN-ATCC 27064 / DSM 738 / NRRL 3585;
MEDLINE-93065223; PubMed-1437568;
                                                                                                                                                                                                                                                                                                                                                                                                 18 OKSRVIENPTEALSVAVEE----GLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 QEEEISEEEAKELDRLVEETKKNGIPWEK 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RSISENSLVAMDFSGQKSRVIENPTEA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40 RSLEENQVVNFDVTHGEGPQAENVSPA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00050; COLDSHOCK.
ProDom; PD000621; Cold_shock; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR002059; Cold_shock.
                                                                                                                                                            EMBL, AE000985; AAB89543.1; -. TIGR; AF1713; -. Hypothetical protein; Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X68245; CAA48316.1; -. PIR; S26378; S26378. PIR; S25584; S25584. HSSP; P41016; 1C90.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.0v
Fre 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 33.35
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00313; CSD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a
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RX PEDENCE FROM N.A.

RX PEDIATE-2138199; PubMed-11780052;

RA Doloukas P. Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Jones M., Stavitdes G., Almeda J.P., Babbage A.K., Bagguley C.L.,

RA Balley J., Barlow K.F., Bates K.N., Berard L.M., Beare D.M.,

RA Basley O.P., Bird C.P., Bladey S.E., Bridgeman A.M., Brown A.J.,

RA Back D., Burtll W.D., Butler A.P., Carder C., Carter N.P.,

Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,

Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,

RA Lington A.G., Frankland J.A., Fraser A., French L., Garner P.,

RA Hunton A.G., Frankland J.A., Eraser A., French L., Garner P.,

RA Hunton A., Hunt A.R., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA M.M. Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.

RA MINE S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,

RA Sune R.M., Shark A., Socht C.E., Sehra H.K., Shownkeen R., Sins S.,

RA Swine C.D., Smith M.L., Socht C.E., Sehra H.K., Shownkeen R., Sins S.,

RA Mitchead S.L., Whittaker P., Walliam S.A., Williams S.A.,

RA Hintehead S.L., Whittaker P., Walliam S.N., Horpe A.,

RA Hintehead S.L., Whittaker P., Walliam S.N., Horpe A.,

RA Hintehead S.L., Whittaker P., Durbin R.W., Bentley D.R., Williams S.A.,

RA Hintehead S.L., Whittaker P., Durbin R.W., Bentley D.R., Beck S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Parathyroid;
WabDinE-97364742; PubMed-9218452;
Collins S.P., Uhler M.D.;
"Characterization of PRI-gamma, a novel isoform of the protein kinase inhibitor of cAMP-dependent protein kinase.";
J. Biol. Chem. 272:18169-18178(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MU U., anau S.;
"Cloning and mapping of human PKIB and PKIG, and comparison of tissue
expression patterns of three members of the protein kinase inhibitor
                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-21060778; Pubmed-10880337;
Zheng L., Yu L., Tu Q., Zhang M., He H., Chen W., Gao J., Yu J.,
Wu Q., Zhao S.;
                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
CAMP-dependent protein kinase inhibitor, gamma form (PKI-gamma).
                                                                                                                                                                                                                                                                        Salto T., Miyajima N.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family, including PKIA.";
Biochem. J. 349:403-407(2000).
                                    STANDARD;
                                                                                                                                                                  sapiens (Human)
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                    NCBI_TaxID=9606;
                              IPKG_HUMAN
Q9Y2B9:
RESULT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Collins S.P., Uhler M.D.,
"Characterization of PKI-gamma, a novel isoform of the protein kinase
"Characterization of PKI-gamma, a novel isoform of the protein kinase
inhibitor of CAMP-dependent protein kinase.";
- FUNCTION: EXTEMBLY BIL18 (1997).
- FUNCTION: EXTEMBLY POTENT COMPETITIVE INHIBITOR OF CAMP-DEPENDENT
- PROTEIN KINASE ACTIVITY, THIS PROTEIN INTERACTS WITH THE
CATALITIC SUBMUNT OF THE ENZYME AFTER THE CAMP-INDUCED
- DISSOCIATION OF ITS REGULATORY CHAINS (BY SIMILARITY).
- SIMILARITY: BELONGS TO THE PKI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
CAMP-dependent protein kinase inhibitor, gamma form (PKI-gamma).
                                                                                                                                                                                                                                                                                                                                                                                           5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
;
                                                                                                                                                                                                                                                                                                                                            17.0%; Score 36; DB 1; Length 76; 31.0%; Pred. No. 4.4e+02; Live 10; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.0%; Score 36; DB 1; Length 76; 31.0%; Pred. No. 4.4e+02; tive 10; Mismatches 8; Indels
                                                                                                                                                                                                                                    MIM; outsz.; ... InterPro; IPRO4171; CAMP_dep_PKI.
Pfam; PF02827; PKI; 1.
Protein kinase inhibitor.
SEQUENCE 76 AA; 7910 MW; F01B4C73ED2CC6EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U97170; AAC09065.1; -.
MGD; MGI:1343086; Pkig.
InterPro; IPR004171; CAMP_dep_PKI.
Profesh: PF02827; PKI; 1.
Protein Kinase inhibitor.
SEQUENCE 76 AA; 7943 MW; 965F577D80C8DE59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              6 SENSLVAMDFSGQKSRV--IENPTEALSV 32
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7 SYSDFISCDRTGRRNAVPDIQGDSEAVSV 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97364742; PubMed-9218452;
                                                                                                                                           EMBL; AB019517; BAA77336.1; --
EMBL; AF182032; AAD55445.1; --
EMBL; 297053; CAC18874.1; --
Genew; HGNC:9019; PKIG.
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 31.0%
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
                                                                                                                                                                                                                             MIM; 604932;
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070139;
                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPKG_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                         Matches
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6 SENSLVAMDFSGQKSRV--IENPTEALSV 32

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GCH1_MUCHA P51598;

RESULT 22

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                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MIDLINE—94359430; PubMed=7915817;

MIDLINE—94359430;

MIDLINE—10.5., Ippen-Thler K., Skurray R.A.;

MIDLINE—11.5. of the sequence and gene products of the transfer region of the F sex factor. The sequence and gene products of the transfer region of Microbiol. Rev. 58:162-210(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shimizu H., Saitch Y., Suda Y., Uehara K., Sampei G., Mizobuchi K.; Complete nucleotide sequence of the F plasmid: Its implications for organization and diversification of plasmid genomes."; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Guanine nucleotide-binding protein G(1)/G(S)/G(O) gamma-T2 subunit
                                                                                                                                            MEDLINE-94292442; PubMed-8021201;
Dozan T.J. Loh S.M., Firth N., Skurray R.A.;
"Molecular analysis of the Fplasmid travR region: trav encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bøvoidea;
       Plasmid F.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Retina;

BODINE-25238332; PubMed-7721746;
ONG O.C., Yamane H.K., Phan K.B., Fong H.K., Bok D., Lee R.H.,
Fung B.K.-K.;
Wholecular cloning and characterization of the G protein gamma subunit of cone photoreceptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Lenye...
No. 4 9e+02;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D2B935EB7CA26137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred, No. 4 9e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                     Bacteriol. 176:4182-4186(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U01159; AAC44209.1; -. EMBL; AP001918; BAA97951.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid; Complete proteome. SEQUENCE 83 AA; 9126 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LVAMDFSGQKSRVIENP 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 IVAYVYKSSRSTVFENP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (G.gamma-C) (G-gamma-8).
GNGT2 OR GNG8 OR GNGT8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        trbg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 7; Conserv
                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9913;
                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GBGU_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EcoGene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gg
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AM MEDLINE-95352066; PubMed-7542887;

MEDLINE-95352066; PubMed-7542887;

Maier J., Witter K., Guetlich M., Ziegler I., Werner T., Ninnemann H.;

Maier J., Witter K., Guetlich M., Ziegler I., Werner T., Ninnemann H.;

RT "Homology cloning of GTP-Cyclohydrolase I from various unrelated

RT "Homology reverse-transcription polymerase chain reaction using a

RT general set of degenerate primers.

RE Glochem. Biophys. Res. Commun. 212:705-711(1995).

CI-CATALYTIC ACTIVITY: GTP + 2 H(2)0 - formate + 2-amino-4-hydroxy-6-

CI-CATALYTIC ACTIVITY: GTP + 2 H(2)0 - formate + 2-amino-4-hydroxy-6-

CI-CATAHUROROLOFPERIN INHIBITS THE BUSYME ACLIVITY (BY SIMILARITY).

CI-CATAHUROROLOFPERIN INHIBITS THE BUSYME ACTIVITY (BY SIMILARITY).

CI-CATAHUROROLOFPERIN DIOSPHANCE ADDISPHANCE ADDISPHANCE OF THE STANDARY ACTIVITY (BY SIMILARITY).

CI-CATAHUROROLOFPERIN SIMILARITY).

CI-CATAHUROROLOFPERIN SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit limitiations as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                          Mucuna hassjoo.
Rukaryota, VIIdiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillionoideae; Phaseoleae; Mucuna.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPRO01474; GTP_cyclohydrol.
Pfam: PF01227; GTP_cyclohydrol; 1.
ProDom; PD003330; GTP_cyclohydrol; 1.
PROSITE; PS00869; GTP_CYCLOHYDROL_1]; PARTIAL.
PROSITE; PS00860; GTP_CYCLOHYDROL_12; 1.
Tetrahydrobiopterin biosynthesis; Hydrolase; Allosteric enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
ق
                                                                                                                                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)'
15-UNN-2002 (Rel. 41, Last annotation update)
GTP Cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 80; Pred. No. 4.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AA; 8845 MW; F5F6C04D2BBDCC36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                          80 AA.
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40.0%;
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                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=40337;
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TRBG_ECOLI P41072;

TRBG_ECOLI

RESULT 23

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Gaps

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Search completed: March 28, 2003, 09:06:02 Job time : 31.4803 secs
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                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration the European the Swiss Institute of Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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J, Biol, Chem. 270:8495-8500(1995).

-1- FUNCTION: GUANINE NUCLEOTIDE-BINDING PROTEINS (G PROTEINS) ARE INVOLVED AS A MODILATOR OR TRANSBOCKER IN VARIOUS TRANSBURBANE SIGNALING SYSTEMS. THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE STRANSBORD OF STRANSBORD FOR THE BETA AND GAMMA CHAINS ARE REQUIRED FOR THE BEFORD INTERACTION.

-1- SUBLINATI G PROTEINS ARE COMPOSED OF 3 UNITS (ALPHA, BETA & GAMMA).

-1- SIMILARITY: BELONGS TO THE G PROTEIN GAMMA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C. SIMILARITY: BELONGS TO THE ATPASE C CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR001770; G-gamma.
InterPro: IPR001770; G-gamma.
InterPro: IPR001310; Prenyl_site.
Ffam; PF00631; G-gamma; 1.
PRINTS; PR00321; GPROTEING.
SWART; SM00224; GGL; 1.
PROSITE; PS50038; G-gamma: 1.
PROSITE; PS50038; G-groverN. GAMMA; 1.
PROSITE; PS50038; G-groverN. GAMMA; 1.
PROSITE; PS50038; G-groverN. GAMMA; 1.
PROSITE; PS50048; G-groverN. GAMMA; 1.
PROPEP 66 66 FRANESYL (BY SIMILARITY).
PROPEP 67 69 REMOVED IN MATURE FORM (BY SIMILARITY).
SBOUENCE 69 AA; 7728 MW; 210C831991520314 CRC64;
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01-APR-1990 (Rel. 14, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ATP synthase protein 9, mitochondrial (EC 3.6.3.14) (Lipid-binding
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9; Mismatches
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Local Similarity 26.5%;
les 9; Conservative
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Pfam; PF00137; ATP-synt_C; 1.
PROSITE; PS00605; ATPASE_C; 1.
Hydrogen ion transport; Lipid-binding; Mitochondrion; CF(0);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.5; DB 1; Length 75; Pred. No. 5.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane.
SEQUENCE 75 AA: 8084 MW; A25519F6F8F1F2F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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PIR; S07730; S07730,
InterPro; IPR002379; APPase_Csub.
InterPro; IPR00454; Eub_ATPase_Csub.
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OM protein - protein search, using sw model  Run on: March 28, 2003, 09:02:45 ; Search time 17.2677 Seconds (without alignments) 239.394 Million cell updates/	:	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 283224 segs, 96134422 residues	Total number of hits satisfying chosen parameters: 22614	Minimum DB seq length: 40 Maximum DB seq length: 90	Max Max Lis Fapire Tapire 2:	1 1
OM protein - protein search, using sw model	March 28, 2003, 09:02:45 ;	. :	March 28, 2003, 09:02:45;  "US-"09-936-697-5	iid	; iid	iid :	r iid

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A; Accession: E64324 A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA A; Residues: 1-76 <bul> A; Cross-references: GB:U67475; GB:L77117; NID:g1590930; PID:g1590941; TIGR:MJ0196; PI C; Genetics: A; Map position: FOR190573-190803 A; Start codon: GTG C; Superfamily: DNA-directed RNA polymerase II chain RPB10 C; Superfamily: DNA-directed RNA polymerase II chain RPB10 C; Superfamily: DNA-directed RNA polymerase; transcription Query Match Guery Match Best Local Similarity 34.4%; Pred. No. 41; Matches II; Conservative 7; Mismatches 12; Indels 2; Gaps 1; Mythosis Similarity Ala, Similarity 11::1 1: 1: 1: 1: 1: 1: </bul>	Cibte: 15-Oct-1999 #text_change 15-Oct-1999 Cibte: 15-Oct-1999 #squence_revision 15-Oct-1999 #text_change 15-Oct-1999 Cibte: 15-Oct-1999 #squence_revision 15-Oct-1999 #text_change 15-Oct-1999 Cibte: 1725/63 Submitted to the EMBL Data Library, February 1997 A;Description: The sequence of C. elegans cosmid F46F11. A;Deference number: 220083 A;Decession: T55/63 A;Decession: T55/64 A;Dec	C.Species: Methanosarcina thermophila C.Species: Methanosarcina thermophila C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 13-Nov-1998 C.Accession: A42960 R;Clements, A.P.; Ferry, J.G. J. Bacteriol. 174, 5244-5250, 1992 A;Title: Cloning, nucleotide sequence, and transcriptional analyses of the gene encod A;Reference number: A42960; MUID:92355496; PMID:1379583 A;Contents: TW.1 A;Accession: A42960 A;Motes sequence extracted from NCBI backbone (NCBIN:110322, NCBIP:110324) A;Residues: 1-60 < CLE> A;Note: sequence extracted from NCBI backbone (NCBIN:110322, NCBIP:110324) C;Genetics: A;Note: sequence extracted from Tansfer; Inon-sulfur protein; metalloprotein C;Genetics: A;Gene: idax C;Superfamily: ferredoxin 2[4Fe-4S] homology C;Keywords: 4Fe-4S; lomology cFER> C;Keywords: 4Fe-4S; lomology cFER> F;10,13,16,51/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
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979 28 13.2 83 2 1 13.2 980 28 13.2 2 84 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 E64510 hypothetical protein MJECL05 - Methanococcus jannaschii plasmid C; Species: Methanococcus jannaschii C; Dete: 13-Sep-1996 #sequence_revision 13-Sep-1996 #sext_change C; Accession: E64510 R; Bult, C.J; When E64510 R; Bult, C.J; White, O.; Olsen, G.J; Zhou, L.; Fleischmann, R.E. scanc, J.D; Sadow, P.W.; Mirkness, E.F.; Weinstock, K.G; Merson, J.D; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M. Sclence 17; Josen 1073, 1996 R; Hilte: Complete genome sequence of the methanogenic archaeon, A; Reference number: A64300; MUID:96337999; PMID:8688087 R; Status: preliminary; nucleic acid sequence not shown; translat A; Mesidens: 1-62 - GML> A; Cross references: GB.L77118; NID:91500644; TIGR:MJECL05; PIDN: C; Genome: plasmid A; Cross references: GB.L77118; NID:91500644; TIGR:MJECL05; PIDN: A; Scanome: plasmid A; Statt codon: GTG A; Mote: this stable 58-kilobase pair plasmid is also designated Ouery Match Dest. Local Similarity 28:08; Score 46.5; DB 2; Length 62; Best. Local Similarity 28:08; Pred. No. 28;	Matches 12; Conservative 8; Mismatches 21, Qy 3 RSISENSLVAMDFS-GOKSRVIENPTBALSVAVEEGCLAWRKK Db 18 KKVAERFIKDLESSOGMDWKEIRERAERAKGLEEGIEWAKK RE434 E6434 DNA-directed RNA polymerase (EC 2.7.7.6) subunit N C; Species: Methanococcus jannaschi C; Species: Methanococcus C; Species: Methanococcus July, Species: Methanococcus July, 10896 A; Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; A; Title: Complete genome sequence of the methanogenic A; Reference number: A64300; MUID:96337999; PMID:86880

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Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PRID:10910347
A;Notes: Tor a complete list of authors see reference number A59328 below.
A;Accession: C82776
A;Status: pro-Liminary
A;Molecule type: DIM.
A;Residues: 1-53 <SIM>A;Residues: 1-53 <SIM>A;Residues: 1-54 <SIM>A;Residues: 1-55 <SIM>A;Ross-references: GBARE003912; GBARE003849; NID:99105560; PIDN:AAF83504.1; GSPDB:(A;Experimental source: strain 9a5c
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              C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: C82776
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide St
Nature 406, 151-157, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STVO-
A;Cross-references: GB:BA000008; NID:g8978582; PIDN:BAA98419.1; GSPDB:GN00142
A;Experimental source: strain J138
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.8%; Score 42; DB 2; Length 53; ilarity 66.7%; Pred. No. 94; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 42; DB 2; Length 79; ilarity 33.3%; Pred. No. 1.5e+02; Conservative 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 FSGOKSRVIENPTEALSVAVEEGL 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 LGVGVERGYAWR 32
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Matches 8; Conserv
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Matches
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R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubols, J.; Aldredge, T.; Ni, Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Witczbowski, J.; Gibson, R.; Jiwani, N. K.; S.; Church, G. M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A6900; MulD:98037514; PMID:931463
                                                                                                                                                                                                                                                                                                                                                                                                                                                             hydrogenase expression/formation protein (hypc) homolog - Archaeoglobus fulgidus Cispecies: Archaeoglobus fulgidus Cispecies: Archaeoglobus fulgidus Cibate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 24-Sep-1999 C;Accession: H69420 R;Klank, H-P. P. Clayton, R.A.; Tomb, J. F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Wetdman, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Nature 390, 364-370, 1997 Ms. Cocayne, J.D.; Weidman, J.F.; McDonald, L. Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C. Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Thlie: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaecd A;Reference number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Wolecule type: DNA
A;Residues: 1-77 <KLE>
A;Cross.references: GB:AE001009; GB:AE000782; NID:92689332; PIDN:AAB89878.1; PID:9264920
C;Superfamily: hydrogenase expression/formation protein hypc
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A;Experimental source: strain Delta H
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hypothetical protein XF0694 [imported] - Xylella fastidiosa (strain 9a5c)
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         21.2%; Score 45; DB 2; Length 60; 42.9%; Pred. No. 43; tive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 45; DB 2; Length 77; llarity 35.1%; Pred. No. 57; Conservative 5; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Indels
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C;Superfamily: hydrogenase expression/formation protein hypc
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                                                                                                                                                                            12 AMDFSGQKSRVIENPTEALSVAVEEGLA 39
                                                                                                                                                                                                                                                         7 ADECSGCGSCVDECPSEAITLDEEKGIA 34
Query Match
Best Local Similarity 42.9%
Matches 12; Conservative
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es 13; Conserv
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profeoglycan core protein, laryngeal cartilage - pig (fragments)
(5, Species: Sus scrofa domestica (domestic pig)
(5, Species: Sus Scrofa domestica (domestic pig)
(5, Accession: A60172
(8, Harris, M.; Kenneally, B.; Barry, F.
Biochem. Soc. Trans. 18, 299, 1990
A; Title: Primary structure of the hyaluronic acid-binding region of porcine laryngeal A; Reference number: A60172; MUID:90337042; PMID:1696222
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C:Keywords: cartilage
F:41-73/Domain: link protein repeat homology (fragment) <LNKl>
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Treel-stimulating antigen - Coccidioides immitis (fragment)
C.Species: Coccidioides immitis
C.Species: Coccidioides immitis
C.Species: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change II-Jan-2000
C.Accession: A43602; S16764
R.Kirkland, T.N.; Zhu, S.; Kruse, D.; Hsu, L.; Seshan, K.R.; Cole, G.T.
A.Title: Coccidioides immitis fractions which are antigenic for immune T lymphocytes.
A.Reference number: A43602; MUID:92040063; PMID:1840578
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A/Molecule type: mRNA
A/Residues: 1.87 <AAL>
A/COSS-references: EMBL:X76604; NID:g471318; PIDN:CAA54065.1; PID:g471319
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                                                                                            Length 82;
                                                                                                                                                                                                                                                            Match 19.6%; Score 41.5; DB 2; Local Similarity 35.1%; Pred: No. 25+02. Local Similarity 35.1%; Pred: No. 25+02. Mismatches 16; Mass 13; Conservative 7; Mismatches 16;
                                                                                                                                                                                                                10 LVAMDFS-GOKSRVIEN-----PTEALSVAVEEGLAWR 41
                                                                                    Score 42; DB 1; 1
Pred. No. 1.6e+02;
8; Mismatches 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 MRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 LRNITGNPEVRVSKMGRAAGVLENHEEGRRYA-EHGL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 QKSRVIENPTEALSVAVEEG-----LAW 40
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Best Local Similarity 32.5%;
Matches 13; Conservative
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A; Residues: 1-73 <HAR>
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es 12; Conserv
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A;Cross references: GB:AE001607; GB:AE001363; NID:g4376474; PIDN:AAD18362.1; PID:g437648
A;Experimental source: strain CWL029
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: B72106
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein CP0557 [imported] - Chlamydophila pneumoniae (strain AR39) C;Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae C;Species: 11-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 R;Red, T.D.; Bruhham, R.C.; Shen, C.; Gill, S.R.; Heidelberg; J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Slazberg, A;Tile; Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MuID:20150255; PMID:10684935
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Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Reach, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, Ison, J.D.; Sadow, P.W.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Schnece 73, 1058-1073, 1996
A. Title: Complete genome sequence of the Mine, Roberts, K.M.; Furst, M.A.
A. Reference number: A64300; MUID:96337999; PMID:8688087
A. Reference number: A64300; MUID:96337999; PMID:8688087
A. Reference number: A64300; MUID:96337999; PMID:8688087
A. Reference number: A64300
A. Stetus: pre-Liminary; nucleic acid sequence not shown; translation not shown
A. Molecule type: DNA
A. Molecule type: DNA
A. Molecule type: G8:UG7505; G8:U77117; NID:92826297; PIDN:AAB98558.1; PID:91591273; T.A. A. Cross-references: G8:U67505; G8:U77117; NID:92826297; PIDN:AAB98558.1; PID:91591273; T.A. Cross-references: G8:U67505-references: G8:U77177; MID:978876297; PID:91591273; T.A. Cross-references: G8:U67505-references: G8:U77177; MID:97897697; PID:91591273; T.A. Cross-references: G8:U77177; MID:97897697; PID:91591273; T.A. Cross-references: G8:U77177; MID:97897697; PID:91591273; T.A. Cross-references: G8:U67505-references: G8:U67505-references: G8:U77177; MID:9159159173; T.A. Cross-references: G8:U67505-references: G8:U77177; MID:9159159173; T.A. Cross-references: G8:U77177; MID:9159173; T.A. Cross-references: G8:U67505-references: G8:U77177; MID:9159173; T.A. Cross-references: G8:U77177; T.A. Cross-references: G8:U77177; T.A. Cross-references: G8:U77177; T.A. Cross-references: G8:U77177; T.
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0567
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C:Species: Methanococcus jannaschii
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
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Best Local Similarity
8; Conserva
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A:Molecule type: DNA
A:Residues: 1-79 <ARN>
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probable transcription regulator homolog lin0437 [imported] - Listeria innocua (str. C; Species : Listeria innocua (Species : Listeria : Li
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S.Species: Nostoc sp.
A.Note: Nostoc sp.
A.Note: Nostoc sp.
C.Species: Nostoc sp.
A.Note: Nostoc sp.
C.Species: Nostoc sp.
A.Note: Nostoc sp.
C.Species: Nostoc sp.
C.Speci
                                                                                                                                                                                                                                                                                                        C; percess accorded actus subsp. ractus (c) bate: 23 Mar-2001 #text_change 03-Aug-2001 (c) bate: 23 Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 (c) Accession: F86696 (c) Accession: F86696 (c) Arithe: 11, 731-753, 2001 (c) Arithe: The complete genome sequence of the lactic acid bacterium Lactococcus lact Arithe: The complete genome sequence of the lactic acid bacterium Lactococcus lact Arecession: F86696 (c) Arithe: The complete genome sequence of the lactic acid bacterium Lactococcus lact Arecession: F86696 (c) Arecession: F86996 (c) Arecession: F
                                                                                                                                                                                                       4-oxalocrotonate tautomerase [imported] - Lactococcus lactis subsp. lactis (strain c; species: Lactococcus lactis subsp. lactis c; becles: Lactococcus lactis subsp. lactis c; bate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%; Score 39.5; DB 2; Length 61; 21.4%; Pred. No. 2.4e+02; Live 14; Mismatches 16; Indels
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Best Local Similarity 21.4%,
Best Some 9; Conservative
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Cipaces: Clostridium acetobutylicum
Cipacession: 697-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
Cipacession: 697-002
RNO111ng, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A; Fitle: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
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G;Species: Wycobacterium tuberculosis

G;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Nov-2000

G;Accession: E70985

R;Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Pevlin, K.; Feltwell, T.; Gentles, S.; Hamiln, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, Y.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A;Authors: Agers, R.; Sulston, D;Aryobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987; PMID:9634230
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A:Experimental source: Clostridium acetobutylicum ATCC824
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A;Residues: 1-70 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                    ö
A):Cross-references: GB:M77190
A):Note: the authors translated the codon ACC for residue 61 as Asn C;Superfamily: human 4-hydroxyphenylpyruvate dioxygenase
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                                                                                                                                                                                                                                                                     Length 66;
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                                                                                                                                                                                                                                                               / Match 18.9%; Score 40; DB 2; local Similarity 26.7%; Pred. No. 2.3e+02; nes 8; Conservative 9; Mismatches
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| EFSALKSIVMASPNDIVKMPINEPAKGKKQ 30
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A; Molecule type: DNA
A; Residues: 1-67 <KUR>
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30S ribosomal subunit protein S22 (imported) - Escherichia coli (strain O157:H7, subs C.Species: Escherichia coli (Species: Escherichia coli (Species: Escherichia coli (Species: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 17-May-2002 (Species: 16-Peb-2001 #sequence_revision 16-Peb-2001 #text_change 17-May-2002 (Species: N.T.: Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May IIIler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda Afttle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
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                                                                                                                  A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and cyleferession: D90809
A;Seference number: A99629; MUD:21156231; PMID:11258796
A;Status: preliminary
A;Solecule type: DNA
A;Solecule type: DNA
A;Coss-references: GB:BA000007; PIDN:BAB35507.1; PID:913361550; GSPDB:GN00154
A;Coss-references: GB:BA000007; PIDN:BAB35507.1; PID:913861550; GSPDB:GN00154
C;Genetics:
A;Gene: ECS2084
C;Superfamily: Escherichia coli ribosomal protein S22
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A; Cross references: EMBL: ALO49656; GSPDB:GN00062; ATSP: T6G15.70
A; Experimental source: cultivar Columbia; BAC clone T6G15
A; Genetics:
A; Gene: ATSP: T6G15.70
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C;Superfamily: Escherichia coli ribosomal protein S22
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Best Local Similarity 29.7%; Pred. No. 2.9e+02;
Matches 11; Conservative 7; Mismatches 19;
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                                                                                8, 11-22, 2001
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Matches 7; Conserv
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A; Status: preliminar
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C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 44-Sep-1999 #sequence_revision 24-Sep-1999 #text_change 01-Mar-2002
C;Accession: C64901
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A Residues: 1-45 < BLAT>
A Experimental source: Strain K-12, substrain MG1655
A Experimental source: Strain K-12, substrain MG1655
A Title: Observation of Escherichia coli ribosomal proteins and their posttranslational A Scherichia coli ribosomal protein with these mass spectrographic characteristics was found; nc C Genetics:
A Geneti
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C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
C; Accession: D90889
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Ruhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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C.Superfamily: Escherichia coli ribosomal protein S22
C.Keywords: protein biosynthesis; ribosome
F:1-45/Product: ribosomal protein S22 #status experimental <MAT>
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A; Reference number: AB1807; MUID;21595285; PMID:11759840
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Matches 8; Conservative
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Mypothetical protein BWEI10182 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Species: Brucella melitensis
C;Accession: AD3532
R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Tille: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD352; PMID:11756688
A;Reference number: AD352; PMID:11756688
A;Reference number: AD352; PMID:11756688
A;Reference number: AD352; PMID:11756688
A;Reference number: AD352; PMID:11756688
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A;Reference number: AD352; PMID:11756688
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C;Date: 15-58p-2000 #sequence_revision 15-58p-2000 #text_change 31-Dec-2000
C;Accession: B83569
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yunn, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MVID:20437337; PMID:10984043
A;Accession: B83269
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A Modecule type: DNA
A Modecule type: DNA
A Status: 1-77 < STO>
A: Residues: 1-77 < STO>
A: Residues: 1-77 < STO>
A: Residues: 1-77 < STO>
A: Caross-references: GB: AE004726; GB: AE004091; NID: g9949108; PIDN: AAG06397.1; GSPDB: GN001
A: Experimental source: strain PAO1
C; Genetics:
A; Gene: PA3009
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A; Experimental source: strain 16M
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3. /Ggn2_G/ptodata/I/pubpaa/USG_NEW_PUB.pep:*

4. /Ggn2_G/ptodata/I/pubpaa/USG_NEW_PUB.pep:*

5. /Ggn2_G/ptodata/I/pubpaa/USG_NEW_PUB.pep:*

6. /Ggn2_G/ptodata/I/pubpaa/USG_NEW_PUB.pep:*

7. /Ggn2_G/ptodata/I/pubpaa/USG_PUBCOMB.pep:*

8. /Ggn2_G/ptodata/I/pubpaa/USG_PUBCOMB.pep:*

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10 US-09-764-872-31

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	Sequence 50, Appl Sequence 374, App Sequence 33369, A Sequence 40621, A			Sequence Sequence Sequence Sequence		Sequence	Sequence			Sequence 36194, A Sequence 37813, A Sequence 47955, A Sequence 47955, A Sequence 75, Appl			Sequence 1911, Ap Sequence 1951, Ap Sequence 48011, A	Sequence 3456 Sequence 3903 Sequence 3516		Sequence 34561, Sequence 1037, A Sequence 1037, A Sequence 39839, Sequence 1037, A Sequence 38332,
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HOFFMAN, No. US20020034755Alh
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KAY, Brian K.
FOWLKES, Dana M.
MCCONNEIL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMANN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
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Local Similarity 26.4%; Pred. No. 24;
Les 14; Conservative 6; Mismatches 7; Indels 26; Gaps
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OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.7
OTHER INFORMATION: EST_HUMAN HIT: BF573955.1, EVALUE 1.60e-02
US-09-864-761-47521
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
                                                                         PRIOR PELING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
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PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
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PRIOR PLING DATE: 2000-06-30
PRIOR PRIOR DATE: 2000-06-30
PRIOR PRIOR DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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TYPE: PRT
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ADDRESSEE: Pennie & Edmonds LLP
STREF: 1155 Avenue of the Americas
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-Jun-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                    PRIOR APPLICATION NUMBER: PCT/US01/00663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 111, Application US/09879957; Patent No. US20020034755A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 2
US-09-879-957-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Sequence 4751, Application US/09864761

Sequence 4751, Application US/09864761

Sequence 47521, Application US/09864761

Sequence 47521, Application US-09864761

Sequence 47521, Application Grant Search Searc
                                                                                                                             Sequence 1224, Ap Sequence 1224, Ap Sequence 39811, A Sequence 45795, A P Sequence 1355, Ap Sequence 35434, A Sequence 35434, A Sequence 35434, A Sequence 5498, Ap Sequence 1113, Ap Sequence 1113, Ap Sequence 1113, Ap Sequence 1113, Ap Sequence 1156, App Sequence 886, App Sequence 
                                Sequence 585, App
Sequence 39691, A
Sequence 49064, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 886, App
Sequence 886, App
Sequence 892, App
Sequence 886, App
Sequence 892, App
Sequence 671, App
Sequence 671, App
        10 US-09-822-827-585

10 US-09-864-761-39691

10 US-09-864-761-39691

10 US-09-864-761-39811

10 US-09-864-761-48090

10 US-09-864-761-45795

10 US-09-864-761-3543

10 US-09-864-761-3543

10 US-09-864-761-3573

10 US-09-864-761-3573

10 US-09-864-761-33789

10 US-09-864-761-33789

10 US-09-864-761-33789

10 US-09-864-761-33789

10 US-09-864-761-33789

10 US-09-796-692-1110

10 US-09-796-692-1120

10 US-09-796-692-1120

10 US-09-796-692-1130

10 US-09-895-793-896

10 US-09-895-793-896

10 US-09-895-793-892

10 US-09-895-814-892

10 US-09-895-814-892
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8; Gaps
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OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL - 74

OTHER INFORMATION: EXPRESSED IN PTACEMAR, SIGNAL - 74

OTHER INFORMATION: EXPRESSED IN BORN BARROW, SIGNAL - 1

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL - 0.82

OTHER INFORMATION: EXPRESSED IN LOUG, SIGNAL - 0.99

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL - 0.99

OTHER INFORMATION: EXPRESSED IN BRIAN, SIGNAL - 0.79

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 0.79

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 0.79

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 0.79

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 1

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 0.79

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 1

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19.8%: Score 42; DB 9; Length 72;
Best Local Similarity 22.0%; Pred. No. 53;
Matches 11; Conservative 12; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 SENSLVAMDFSGQKSRVI-----ENPTEALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 SQVGLPILYFSGRRERLLLRPEVLAEIPREAFTVE----AWVK 51
          PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34262
LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REPERENCE: 249-125
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/99/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR PRILING DATE: 2000-08-03
NUMBER OF SED ID NOS: 7059
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US-09-738-626-6764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6764, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : NAKAGAWA, SATOSHI
: MIZOGUCHI, HIROSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Conservative
                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Hanzel, David K.
APPLICANT: Howen Will K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 20.5%; Score 43.5; DB 10; Length 55; Best Local Similarity 41.4%; Pred. No. 23; Matches 12; Conservative 8; Mismatches 4; Indels
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE OF INVENTION. GENE EASTESSOUN AND STATE OF THE PERFENDE. ACCUREEN TAPPLICATION NUMBER: US/09/864,761 CURRENT FILME DATE: 2001.05-23 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 09/632,366 PRIOR FILING DATE: 2000-05-03 PRIOR APPLICATION NUMBER: GB 24263.6 PRIOR PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: «Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-09-879-957-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00669
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APPLICATION NUMBER: PCT/US01/00664
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LICATION NUMBER: PCT/US01/00666
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FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::: ||||: || ||::| | || ||:
23 TVNKGSLVALGFSDGQEAR----PEEILN 47
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FILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 09/774, 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34262, Application US/09864761
Patent No. US20020048763A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-864-761-34262
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APPLICATION NUMBER: PCT/US98/13684
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RIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-07-08

RIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

RIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

RIOR FLILNG DATE: EARLIER FILING DATE: 1997-07-09

RIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER FILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER FILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER PAPLICATION NUMBER: 60/051, 916

RIOR FILING DATE: EARLIER PAPLICATION NUMBER: 60/051, 916

RIOR PILING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR PLING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR PLING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR PLING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR APPLICATION NUMBER: EARLIER RAPLICATION NUMBER: 60/051, 920

RIOR PILING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR PILING DATE: EARLIER PAPLICATION NUMBER: 60/051, 920

RIOR PILING DATE: EARLIER PILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER PILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER PILING DATE: 1997-07-08

RIOR PILING DATE: EARLIER PILING DATE: 1997-08-18

RIOR PILING DATE: EARLIER PILING DATE: 1997-08-
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR PELLING DATE: EARLIER PELLING DATE: 1997-07-08
PRIOR PELLING DATE: EARLIER FILING DATE: 1997-07-08
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PRIOR PELLING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR PELLING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR PELLING DATE: EARLIER PELLING DATE: 1997-08-18
PRIO
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CURRENT APPLICATION NUMBER: US/09/983,802
CURRENT APPLICATION NUMBER: US/09/983,802
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-07
PRIOR PELING DATE: EARLIER FILING DATE: 1997-07-07
PRIOR PILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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APPLICATION UNDHER: 60/051,926
DATE: 1997-07-08
APPLICATION NUMBER: 60/052,793
DATE: 1997-07-08
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PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
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DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
                         12 AMDF-SGQKSRVIENPTEALSVAVEEGLAWR 41
                                                                Sequence 611, Application US/09983802
Publication No. US20030022185A1
GENERAL INFORMATION:
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OTHER INFORMATION: EXPRESED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: EXPRESED IN PETAL LIVER, SIGNAL = 1.3
OTHER INFORMATION: WISSPROY HIT: R15413.1, EVALUE 2:00e-22
US-09-864-761-41352
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Mismatches
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OTHER INFORMATION: MAP TO ALL58049.2
OTHER INFORMATION: EXPRESSED IN LUNG,
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Matches 12; Conserv
-09-864-761-41352
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, David R.
APPLICANT: Penn, David R.
APPLICANT: Penn, David R.
APPLICANT: Chor, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Accomica.x-1
CURRENT APPLICATION NUMBER: US/O9/864,761
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLILING DATE: 2000-02-04
PRIOR PLILING DATE: 2000-02-04
PRIOR RILLING DATE: 2000-05-26
PRIOR RILLING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . LOCATION: (58)
CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-872-331
                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.9%; Score 40; DB 9; Length 71; 44.0%; Pred. No. 1e+02; trive 3; Mismatches 5; Indels
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-36
PRIOR FILING DATE: 2000-08-36
PRIOR FILING DATE: 2000-09-40
PRIOR PLILING DATE: 2000-09-40
PRIOR PLILING DATE: 2000-09-27
PRIOR PLILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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Patent No. US20020048763A1
GENERAL INFORMATION:
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               NUMBER OF SEQ ID NOS: 957
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 351
TANGTH: 71
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Best Local Similarity 44.09
Matches 11; Conservative
                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (52)
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
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CURRENT APPLICATION NUMBER: US/09/764,872
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 18.9%; Score 40; DB 9; Length 63; Best Local Similarity 47.1%; Pred. No. 86; Matches 6; Indels Matches 6; Indels
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US-09-895-913A-280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kleanthous, Harold APPLICANT: Al-Garawi, Amal
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Best Local Similarity 25.0°
"-+shes 8; Conservative
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US-09-983-802-611
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US-09-764-872-351
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Query Match
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Best Local Similarity 32.4%; Pred. No. 1.18+02;
Matches 11; Conservative 8; Mismatches 14; Indels 1; Gaps
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ITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PALI3
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper SOGITWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.6%; Score 39.5; DB 10; Length 78; 36.4%; Pred. No. 1.3e+02; tive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AC005083.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.5
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.49
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
US-09-864-761-47104
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APPLICANT: 2yskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
                            PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
FRANCE: 2010 NO 47104
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CURRENT APPLICATION NUMBER: US/09/815,242
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Patent No. US20020061569A1
GENERAL INFORMATION:
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Patent No. US20020042096Al
GENERAL INFORMATION:
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Best Local Similarity 36.48
                                                                                                                                                                                                             ORGANISM: Homo sapiens
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US-09-764-887-218
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US-09-815-242-4918
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US-09-764-887-218.
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; Patent No
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GURREMAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TILLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FO

FILE REPERENCE: ACONTON: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FO

CURRENT PILLING DATE: 2000-05-23

PRIOR FILLING DATE: 2000-05-34

PRIOR FILLING DATE: 2000-05-26

PRIOR PELICATION NUMBER: US 60/20/456

PRIOR PELICATION NUMBER: US 60/236,359

PRIOR FILLING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR PELICATION NUMBER: PCT/US01/00666

PRIOR FILLING DATE: 2001-01-30

PRIOR PELICATION NUMBER: PCT/US01/00669

PRIOR PELICATION NUMBER: PCT/US01/00669

PRIOR PELICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

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PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR PELING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELING DATE: 2001-01-30

PRIOR PELICATION NUMBER: PCT/US01/00668

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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER: 60/269,308
PRIOR PILING DATE: 2001-02-16
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00661
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APPLICATION NUMBER: PCT/US01/00661
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Patent No. US20020048763A1
GENERAL INFORMATION:
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les 11; Conserva
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US-09-864-761-43815
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APPLICANT: Rank, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
TITLE OF INVENTION: HUMAN GENOME SINGLE EXON NUCLEIC ACID PROBES USEFUL F
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR PELING DATE: 2000-06-03
PRIOR PELING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: GB 242636
PRIOR APPLICATION NUMBER: CB 242636
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
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CTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.77
CTHER INFORMATION: EXPRESSED IN BODE MARROW, SIGNAL = 0.65
COTHER INFORMATION: EXPRESSED IN BODE MARROW, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.74
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.48
OTHER INFORMATION: ST.HUMAN HIT: AV756022.1, EVALUE 6.00e-20
US-09-864-761-45291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.4%; Score 39; DB 10; Length 60; Best Local Similarity 33.3%; Pred. No. 1.1e+02; Matches 7; Conservative 7; Mismatches 7; Indels
       PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 20001-01-30
PRIOR PLILING DATE: 20001-01-30
PRIOR PLILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2000-09-31
PRIOR FILING DATE: 2001-01-29
NUMBER: QF SEQ ID NOS: 49117
SEQ ID NO 45291
SEQ ID NO 45291
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Sequence 36073, Application US/09864761
Patent No. US20020048763A1
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Aecomica * X · 1
CURRENT APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/180, 312
PRIOR APPLICATION NUMBER: US 60/207, 456
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR APPLICATION NUMBER: US 60/236, 356
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-06-03
PRIOR FILING DATE: 2000-09-06-03
PRIOR FILING DATE: 2000-09-06-03
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2001-01-00
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN DUNG, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.76
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.76
US-09-864-761-43815
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR RILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTHARE: Annomax Sequence Listing Engine vers: 1.1
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LVAMDFSGQKSRVIENPTEALSV 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 43815
LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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9; Mismatches
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FILING DATE: CURNOWN>ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LVAMDFSGQKSRVIENPTEALSVAVEEGL 38
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 301, Application US/09939980; Patent No. US20020008234A1
GENERAL INFORMATION: APPLICANT: Black, Michael
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TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Black, Michael
Burnham, Martin
Hodgson, John
Knowles, David
Lonetto, Michael
                                                                 8; Conservative
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Best Local Similarity
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US-09-939 4980-301
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US-09-925-300-1560
                                                                 Matches
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 6.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 7.8
OTHER INFORMATION: EXPRESSED IN BEAL, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN HEAL, SIGNAL = 6.8
OTHER INFORMATION: EXPRESSED IN HEAL, SIGNAL = 6.5
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 8.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.7
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 6.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN EXPLAINED THE 2.00e-31
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Best Local Similarity 25.8%; Pred. No. 2.1e+02;
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APPLICANT: Mathews, Helena
APPLICANT: Liu, Xing Liang
APPLICANT: Liu, Xing Liang
APPLICANT: Waggoner, Wency J.
TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
TITLE OF INVENTION: METHOD
                                   PRIOR FILING DATE: 2001-01-30
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/0662
PRIOR PILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR PELICATION NUMBER: PCT/US01/0060
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-02-1
PRIOR FILING DATE: 2000-02-1
PRIOR PILING DATE: 2000-08-30
PRIOR PILING DATE: 2000-08-30
PRIOR PELING DATE: 2000-08-30
PRIOR PILING DATE: 2000-08-30
PRIOR PELING DATE: 2000-08-30
PRIOR PELING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 4917-
SEOTTMARE: Annomax Sequence Listing Engine vers: 1.1
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US-09-522-334-28
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CURRENT FILING DATE: 2000-03-09
PRIOR APPLICATION NUMBER: US 60/124,232
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 85
PRIOR APPLICATION NUMBER: PCT/US01/00663
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 11; Conserva
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SEQ ID NO 36073
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Nicholas, Michard
Pratt, Julie
Reichard, Richard
Rosenberg, Martin
Nard, Judith
TITLE OF INVENTION: No. US20020082234Alel Prokaryotic Polynucleotides,
Polypeptides and Their Uses
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  Gaps
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13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
COUNTRY: USA
ZIP: 1946-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: TESTER: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,980
FILING DATE: 27-Aug-2001
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 62 amino acids
TYPE: amino acidd
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 301:
US-09-939-980-301
                            14 DFSGQKSRVIENPTEALS-VAVEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE, DOCKET NUMBER: P50549
                                                           15 NFSSNETELLRRQFDLASREAMDESAVWRKR 45
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; LOCATION: (26)
.; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-225-300-1765
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APPLICANT: Crain Rosen,
APPLICANT: Crain Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR PLILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1899
SEQ ID NOS: 1890
SEQ ID NO 1765
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                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.77

OTHER INFORMATION: EXPRESSED IN PACKETY, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.83

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71

OTHER INFORMATION: SWISSPROT HIT: P49643, EVALUE 1.00e-21
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  PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PAPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 43411
LENGTH: ALLONG SEQUENCE LISTING Engine vers: 1.1
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Patent No. US20020151681A1
GENERAL INFORMATION:
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; Sequence 735, Application US/10092154
; Publication No. US20030054375A1
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nes 12; Conservative
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Matches 9; Conservative
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US-09-925-300-1765
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Matches
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APPLICANT: Ranh, David R.
APPLICANT: Then, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                    APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
APPLICANT: Craig Rosen,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies,
FILE REFERENCE: PAIO1
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
FRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.9%; Score 38; DB 10; Length 68; 34.6%; Pred. No. 1.9e+02; tive 5; Mismatches 12; Indels
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-06
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-03
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PRIOR FILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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Patent No. US20020048763A1
GENERAL INFORMATION:
Sequence 1560, Application US/09925300 Patent No. US20020151681A1 GENERAL INFORMATION:
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Best Local Similarity 34.6*
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US-09-864-761-43411
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94111-3834
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les 11; Conserva
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APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 AMDFS-GOKSRVIENPTE------ALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                            7 AMKFSKNQKYFVLELPSEDVKLVNIKTTVQFITNHFPLPVATKSSLSFQK 56
            APPLICANT: ROSE et al.
TTLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PROUGCI CURRENT APPLICATION NUMBER: US/10/092,154
NUMBER OF SEQ ID NOS: 2003
Prior Application removed - See File Wrapper or Palm SEQ ID No 735
LENGTH: 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PERDICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REPERENCE: PA105
CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
PRIOR PILING DATE: 2000-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 2001-03-08
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 735, Application US/09764847
Patent No. US20020132767A1
GENERAL INFORMATION:
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Patent No. US20020081659A1
GENERAL INFORMATION:
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Matches 15, Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 543
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                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-10-092-154-735
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US-09-764-847-735
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; ORGANISM: Homo sapiens
US-09-925-297-543
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es 15; Conserva
GENERAL INFORMATION;
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APPLICANT: Harada, John
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
CORRESPONDENCE ADDRESS: 324
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Patent No. US20020147140a1
Patent No. US20020147140a1
Patent No. US20020147140a1
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
Ouery Match
Best Local Similarity 27.0%; Pred. No. 3.1e+02;
Matches 10; Conservative 9; Mismatches 15;
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COMBUTER: IDM PC Compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DARA:
FILING DATE: UD-MAY-1998
CLASSIFTCATION: 800
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Two Embarcadero Center, Eighth Floor
San Francisco
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                                                                                                                                                                                                                                                        Sequence 294, Application US/09071838 Patent No. US20020152501A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                Fischer, Robert L.
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Kiyosue, Tomohiro
Yadegari, Ramin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 294:
SEQUENCE CHARACTERISTICS:
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Search completed: March 28, 2003, 09:19:16 Job time : 22.8819 secs

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Sequence Seq	Sequence 39 Sequence 1, Sequence 6, Sequence 16 Sequence 16 Sequence 10 Sequence 2, Sequence 2,
105-09-528-706-56 Sequence US-08-167-035-29 Sequence US-08-169-537A-9 Sequence US-08-6469-537A-9 Sequence US-08-6469-537A-9 Sequence US-08-59-005-29 Sequence US-08-237-401A-2 Sequence US-08-237-401A-2 Sequence US-08-237-401A-2 Sequence US-08-237-401A-2 Sequence US-08-237-401A-2 Sequence US-08-259-514-5 Sequence US-08-259-514-5 Sequence US-08-259-514-5 Sequence US-08-217-249-167 Sequence US-08-217-249-167 Sequence US-08-217-249-167 Sequence US-08-218-115-5 Sequence US-08-218-113-115-5 Sequence US-08-218-113-115-5 Sequence US-08-218-113-115-5 Sequence US-08-218-113-115-5 Sequence US-08-218-218-218-218-218-218-218-218-218-21	S-08-279-127-1 Sequence 39 Sequence 39 Sequence 30 Sequence 1, Sequence 2, S-08-070-155-2 Sequence 2, S-08-0134-001C-5426 Sequence 2, Sequence 5, Se
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15.6 54 1 US-09-528-706-56 Sequence 15.6 54 1 US-09-528-706-59 Sequence 15.6 54 1 US-08-167-035-29 Sequence 15.6 54 1 US-08-167-035-29 Sequence 15.6 54 2 US-08-167-035-29 Sequence 15.6 54 2 US-08-168-19 Sequence 15.6 59 2 US-08-168-19 Sequence 15.6 59 1 US-08-17-010-8 Sequence 15.6 69 1 US-08-17-010-8 Sequence 15.6 69 1 US-08-17-010-8 Sequence 15.3 10 US-08-17-011-9 Sequence 15.3 10 US-08-17-011-9 Sequence 15.3 10 US-08-17-011-9 Sequence 15.3 1 US-08-17-011-9 Sequence 15.3 1 US-08-17-11-9 Sequence 15.3 1	15.1 74 1 US-08-130-731A-39 Sequence 39 15.1 74 1 US-08-29-127-1 Sequence 39 15.1 78 4 US-08-293-502-6 Sequence 1, 15.1 78 5 PCT-US95-10521-6 Sequence 1, 15.1 83 4 US-09-382-155-16 Sequence 16, 15.1 84 4 US-09-145-558-10 Sequence 16, 15.1 87 1 US-08-070-165F-2 Sequence 10, 15.1 87 2 US-08-070-165F-2 Sequence 2, 15.1 87 2 US-08-070-165F-2 Sequence 2, 15.1 90 4 US-09-134-001C-5426 Sequence 54, 15.1 90 4 US-09-134-001C-5426 Sequence 54, 15.1 90 4 US-09-134-001C-5426
6 50 4 US-09-528-706-56 Sequence 6 54 1 US-08-167-035-29 Sequence 6 54 1 US-08-167-035-29 Sequence 6 54 2 US-08-469-537A-3 Sequence 54 2 US-08-469-537A-3 Sequence 54 4 US-09-346-5108-18 Sequence 55 2 US-08-410-804-5 Sequence 55 2 US-08-410-804-5 Sequence 6 59 1 US-08-528-11-5 Sequence 6 59 1 US-08-528-11-5 Sequence 59 1 US-08-538-11-5 Sequence 59 1 US-08-538-543-1 Sequence 50 1 US-08-538-543-1 Sequence 50 1 US-08-538	15.1 74 1 US-08-130-731A-39 Sequence 39 15.1 74 1 US-08-29-127-1 Sequence 39 15.1 78 4 US-08-293-502-6 Sequence 1, 15.1 78 5 PCT-US95-10521-6 Sequence 1, 15.1 83 4 US-09-382-155-16 Sequence 16, 15.1 84 4 US-09-145-558-10 Sequence 16, 15.1 87 1 US-08-070-165F-2 Sequence 10, 15.1 87 2 US-08-070-165F-2 Sequence 2, 15.1 87 2 US-08-070-165F-2 Sequence 2, 15.1 90 4 US-09-134-001C-5426 Sequence 54, 15.1 90 4 US-09-134-001C-5426 Sequence 54, 15.1 90 4 US-09-134-001C-5426

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12.7 56 4 US-09-058-459-63 Sequence 6 12.7 56 4 US-09-058-459-64 Sequence 6 12.7 56 4 US-09-058-459-66 Sequence 6 12.7 56 4 US-09-058-459-66 Sequence 6 12.7 56 4 US-09-058-459-79 Sequence 6 12.7 56 4 US-09-058-459-79 Sequence 7 12.7 56 4 US-09-127-926-41 Sequence 7 12.7 56 4 US-09-127-926-41 Sequence 5 12.7 56 4 US-09-127-926-41 Sequence 5 12.7 56 4 US-09-127-926-51 Sequence 6 12.7 56 4 US-09-127-926-51 Sequence 7 US-09-127-926-51 Sequence 6 12.7 56 4 US-09-127-926-51 Sequence 7 US-09-127-926-51 Sequence	12.7 56 4 US-09-127-926-91 Sequence 90, 12.7 56 4 US-09-127-926-92 Sequence 91, 12.7 56 4 US-09-127-926-92 Sequence 91, 12.7 56 4 US-09-127-926-95 Sequence 92, 12.7 56 4 US-09-127-926-97 Sequence 92, 12.7 56 4 US-09-127-926-97 Sequence 93, 12.7 56 4 US-09-127-926-97 Sequence 97, 12.7 56 4 US-08-93-771-77 Sequence 97, 12.7 57 3 US-08-93-128 Sequence 158, 12.7 57 3 US-08-919-59-158 Sequence 158, 12.7 57 3 US-08-919-597-158 Sequence 158, 12.7 57 3 US-08-919-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-918-918-918-918-918-918-918-918-91
Sequence 6 4 US-09-058-459-63 Sequence 6 4 US-09-058-459-65 Sequence 6 5 4 US-09-058-459-65 Sequence 6 5 6 4 US-09-058-459-65 Sequence 6 5 6 4 US-09-058-459-65 Sequence 6 5 6 4 US-09-058-459-71 Sequence 7 US-09-058-459-72 Sequence 7 US-09-058-459-73 Sequence 7 US-09-127-926-43 Sequence 7 US-09-127-926-43 Sequence 7 US-09-127-926-43 Sequence 7 US-09-127-926-43 Sequence 7 US-09-127-926-44 Sequence 7 US-09-127-926-43 Sequence 7 US-09-127-926-44 Sequence 7 US-09-127-926-45 Sequence 7 US-09-127-926-45 Sequence 5 US-09-127-926-55 Sequence 5 US-09-127-926-56 Sequence 5 US-09-127-926-56 Sequence 5 US-09-127-926-56 Sequence 5 US-09-127-926-56 Sequence 6 US-09-127-926-56 Sequence 7 US-09-127-926-56 Sequence 6 US-09-127-926-57 Sequence 6 US-09-127-926-57 Sequence 6 US-09-127-926-57 Sequence 6 US-09-127-926-57 Sequence 7 US-09-127-926-59 Sequence 7 US-09-127-926-59 Sequence 7 US-09-127-926-59 Sequence 6 US-09-127-926-59 Sequence 7 US-09-127-926-59 Sequence 7 US-09-127-926-69 Sequence 7 US-09-127-926-93 Sequence 8 US-09-127-926-93 Sequ	12.7 56 4 US-09-127-926-91 Sequence 90, 12.7 56 4 US-09-127-926-92 Sequence 91, 12.7 56 4 US-09-127-926-92 Sequence 91, 12.7 56 4 US-09-127-926-95 Sequence 92, 12.7 56 4 US-09-127-926-97 Sequence 92, 12.7 56 4 US-09-127-926-97 Sequence 93, 12.7 56 4 US-09-127-926-97 Sequence 97, 12.7 56 4 US-08-93-771-77 Sequence 97, 12.7 57 3 US-08-93-128 Sequence 158, 12.7 57 3 US-08-919-59-158 Sequence 158, 12.7 57 3 US-08-919-597-158 Sequence 158, 12.7 57 3 US-08-919-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-138, 12.7 57 3 US-08-918-918-918-918-918-918-918-918-918-91
12.7 56 4 US-09-058-459-63 Sequence 6 12.7 56 4 US-09-058-459-64 Sequence 6 12.7 56 4 US-09-058-459-66 Sequence 6 12.7 56 4 US-09-058-459-66 Sequence 6 12.7 56 4 US-09-058-459-79 Sequence 6 12.7 56 4 US-09-058-459-79 Sequence 7 12.7 56 4 US-09-127-926-41 Sequence 7 12.7 56 4 US-09-127-926-41 Sequence 5 12.7 56 4 US-09-127-926-41 Sequence 5 12.7 56 4 US-09-127-926-51 Sequence 6 12.7 56 4 US-09-127-926-51 Sequence 7 US-09-127-926-51 Sequence 6 12.7 56 4 US-09-127-926-51 Sequence 7 US-09-127-926-51 Sequence	27 12.7 56 4 US-09-127-926-91 Sequence 90, 27 12.7 56 4 US-09-127-926-91 Sequence 91, 27 12.7 56 4 US-09-127-926-92 Sequence 91, 27 12.7 56 4 US-09-127-926-95 Sequence 92, 27 12.7 56 4 US-09-127-926-97 Sequence 92, 27 12.7 56 4 US-09-127-926-97 Sequence 97, 27 12.7 56 4 US-09-127-926-97 Sequence 97, 27 12.7 56 4 US-08-823-771-77 Sequence 97, 27 12.7 57 3 US-08-919-918-918-918-918-918-918-918-918-91

Sequence 20, Appl Sequence 4, Appl Sequence 68, Appl Sequence 68, Appl Sequence 68, Appl Sequence 68, Appl Sequence 786, Appl Sequence 187, Appl Sequence 35, Appl Sequence 35, Appl Sequence 35, Appl Sequence 37, Appl Sequence 118, Appl Sequence 999, Appl Sequence 999, Appl Sequence 999, Appl Sequence 999, Appl Sequence 5, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 5, Appl Sequence 54,	011001 000001010101414
4 US-09-193-931C-20 US-08-174-632-4 US-08-174-632-4 US-08-174-174A-4 US-09-227-357-580 US-09-227-357-580 US-09-315-304B-786 E	4 US-09-082-279B-998 4 US-09-082-279B-998 4 US-09-315-304B-995 4 US-09-315-304B-995 4 US-09-315-304B-1089 4 US-09-315-304B-1089 5304637-13 1 US-08-625-322-23 1 US-08-625-322-23 1 US-08-484-223B-994 4 US-09-315-304B-994 1 US-08-290-919-1 1 US-08-290-919-1 1 US-08-290-919-1 4 US-09-315-304B-1090 4 US-09-315-304B-1090 4 US-09-315-304B-1090 4 US-09-315-304B-1090 5 US-08-290-071-4 6 US-09-315-304B-1090 6 US-09-315-304B-1090 7 US-09-315-304B-1090 8 US-09-315-304B-1090 8 US-09-315-304B-1090 8 US-09-315-304B-1090 8 US-09-315-304B-1090 8 US-09-315-304B-1090 8 US-09-315-304B-1090
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Sequence 2, Appli Sequence 6, Appli Sequence 14, Appli Sequence 18, Appli Sequence 11, Appli Sequence 14, Appli Sequence 15, Appli Sequence 10, Appli Sequence 21, Appli Sequence 23, Appli Sequence 11, Appli Sequence 15, Appli Sequence 11, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli Sequence 15, Ap	
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	1 US-008-321-01A-20 Sequence US-008-321-01A-20 Sequence US-09-306-446C-13 Sequence US-09-306-446C-13 Sequence US-09-306-446C-13 Sequence US-09-300-672-7 US-08-20-672-671 Sequence US-09-106-56BE-103 Sequence US-09-106-56BE-103 Sequence US-09-104-476-671 Sequence US-09-104-476-671 Sequence US-09-134-001C-28BB Sequence US-09-134-001C-28BB Sequence US-09-441-151-39 Sequence US-09-40-151-39 Sequence US-09-136-20-21 Sequence US-09-136-20-21 Sequence US-09-136-20-21 Sequence US-09-136-20-21 Sequence US-09-136-20-21 Sequence US-09-136-20-21 Sequence US-09-136-30-20-21 Sequence US-09-136-30-20-21 Sequence US-09-134-37-8 Sequence US-09-134-41-818-22 Sequence US-09-134-41-818-22 Sequence US-09-134-478-20 Sequence US-09-134-41-818-22 Sequence
12.7 83 US-08-852-865-2 Sequence 27 12.7 83 US-08-991-988A-6 Sequence 27 12.7 83 PCT-0593-10069-24 Sequence 27 12.7 85 2 US-08-525-664A-18 Sequence 27 12.7 85 1 US-08-525-664A-18 Sequence 27 12.7 86 1 US-09-165-422-18 Sequence 27 12.7 86 1 US-09-165-422-18 Sequence 27 12.7 86 1 US-09-165-422-18 Sequence 27 12.7 86 1 US-09-165-422-14 Sequence 27 12.7 86 1 US-09-411-56-14 Sequence 27 12.7 86 1 US-09-411-82 Sequence 27 12.7 86 1 US-09-411-82 Sequence 27 12.7 86 1 US-09-411-82 Sequence 28 1 US-09-411-82 Sequence Sequence 29 1 US-09-414-13 Sequence	12.5 54 1 US-0B-31.0TJA-20 Sequence 12.5 54 2 US-0B-319.866-3 Sequence 12.5 54 4 US-09-306-446C-13 Sequence 12.5 58 2 US-09-306-72-18-58 Sequence 12.5 60 4 US-09-672-75-58 Sequence 12.5 60 4 US-09-106-765-18 Sequence 12.5 60 4 US-09-106-765-1 Sequence 12.5 64 4 US-09-114-401 Sequence 12.5 64 4 US-09-114-401 Sequence 12.5 65 3 US-09-314-401 Sequence 12.5 65 3 US-09-314-501 Sequence 12.5 65 3 US-09-314-55A-39 Sequence 12.5 66 4 US-09-314-56A-34 Sequence 12.5 67 1 US-09-34-35A-35 Sequence 12.5 67 1 US-09-34-35A-36

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Gaps
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| Patent No. 6093544
| GENERAL INFORMATION:
| APPLICANT: Gonsalves, Dennis APPLICANT: Gonsalves, Dennis APPLICANT: Gonsalves, Dennis APPLICANT: Mongy, Boachong TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES CORRESPONDENCE ADDRESS: 54
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051
Ouery Match 20.8%; Score 44; DB 4; Length 47; Best Local Similarity 34.8%; Pred. No. 8; Matches 8; Conservative 7; Mismatches 8; Indels
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APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, BIAIN K.
APPLICANT: KAY, BIAIN K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: POWLES, Dana M.
APPLICANT: POWLED, Stephen J.
TITLE OF INVENTION: DOLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Sequence IN. 6721368
GENERAL INCORMATION:
APPLICANT: LENTZEN, Hans
APPLICANT: BAUK, Axel
APPLICANT: ZINKE, Holgen
APPLICANT: ENTRE, HOLGEN
TITLE OF INVENTION: RECOMBINANT MISTLETOE LECTIN (RML)
FILE REFERENCE: 674503-2003 .
CURRENT APPLICATION NUMBER: US/08/776,059B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUBER: US/08/630,915A FILING DATE: 03-APR-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.5%; Score 43.5; Di
Best Local Similarity 41.4%; Pred. No. 12;
Matches 12; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 SISENSLVAMDFS-GOKSRVIENPTEALS 31
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                                                                                                                                                                       Sequence 111, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
             19 KSRVIEN--PTEALSVAVEEGLAWRK 42
                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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                                                                                                                              RESULT 6
US-08-630-915A-111
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                                   Gaps
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                                                                                                                                                                                                                                                                                                   APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
APPLICANT: Mang, Baczhong
TITLE OF INVENTION: RUDESTRIS STEM PITTING ASSOCIATED VIRUS
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
FILE REFERENCE: 07678/035005
CURRENT APPLICATION NUMBER: 05/09/574,141A
PRIOR FILING DATE: 1997-05-10
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR PILING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 97
SOFTHARE: FEASTSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
TYTLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
FILE REFERENCE: 07678/035006
CURRENT FILIKE DATE: 2000-11-07
PRIOR PILING DATE: 1998-05-19
PRIOR PILING DATE: 1998-05-19
PRIOR PILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-12-17
NUMBER OF SEQ ID NOSS: 54
NUMBER OF SEQ ID NOSS: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT ... ORGANE: Rupestris stem pitting associated virus US-09-707-780-20
Best Local Similarity 50.0%; Pred. No. 17; Matches 13; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
                                                                           19 KSRVIEN--PTEALSVAVEEGLAWRK 42
                                                                                                         US-09-574-141A-20
Sequence 20, Application US/09574141A
Patent No. 6395490
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 KSRVIEN--PTEALSVAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09707780 Patent No. 6399308
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Best Local Similarity 50.0°
Matches 13; Conservative
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SEQ ID NO 20
LENGTH: 80
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1 PMRSISENSLVAMDFSGQKSRVIENPTE 28
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REGISTRATION NUMBER: 36,170
REPERENCE/POCKET NUMBER: 4-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-277-3368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO FRAGMENT TYPE: N-terminal US-07-781-248A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 908-277-4306
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 40 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                       New Jersey
USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                      Summit
                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                       US-07-781-248A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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US-08-459-568-52
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APPLICANT: Mossalayi, Mohammed D
TITLE OF INVENTION: A PHARMACEUTICAL PREPARATION FOR THE
TITLE OF INVENTION: MATURATION OF PROTHYMOCYTES
TORRESPONDENCE: GCORRESPONDENCE: GCORRESPONDENCE ADDRESS:
ADDRESSEE: Irving M. Fishman, CIBA-GEIGY Corporation
STREET: 556 MORTIS Avenue
                                                                                                                                                                                                                                          Ouery Match
19.8%; Score 42; DB 4; Length 47;
Best Local Similarity 30.8%; Pred. No. 16;
Matches 8; Conservative 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 1; Length 40;
Pred. No. 19;
5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: #PELICATION NUMBER: US/07/641,971B
CURRENT FILING DATE: 1999-06-19
EARLIER APPLICATION NUMBER: PCT/EP96/02273
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 93109949.8
EARLIER FILING DATE: 1995-06-26
NUMBER OF SEQ ID NOS: 56
SEQ ID NO. 16
LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-17921/+/DEB
                                                                                                                                                                                                                                                                                                                    10 LVAMDFSGQKSRVIENPTEALSVAVE 35
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3 LTFMEAVNKKARVVKNEARFLLIAIQ 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/07641971B
Patent No. 5236706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90016254
FILLING DATE: 24-JAN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                      ; ORGANISM: Saponaria officinalis
US-08-776-059-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fishman, Irving M
REGISTRATION NUMBER: 30258
REFERENCE/COCKET NUMBER: 4-1
TELECOMMUNICATION:
TELEPHONE: 908-277-4832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 908-277-4306
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 39.3%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
US-07-641-971B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 40 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summit:
New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CLASSIFICATION:
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US-07-641-971B-5
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4; Gaps
                                                                                                                 Sequence 5. Application US/07781248A
Patent No. 5246699.
GENERAL INFORMATION
APPLICANT: Debre, Patrice
APPLICANT: Mossalavi, Mohammed D
TITLE OF INVENTION: MATURATION OF HEMATOPOIETIC CELLS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: ITVING M. Fishman, CIBA-GEIGY Corporation
STREET: 556 Morris Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES, 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 19.3%; Score 41; DB 1; Length 40; Best Local Similarity 39.3%; Pred. No. 19; Matches 11; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PELLICATION NUMBER: US/07/781,248A
FILING DATE: 19911230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-18065/A/DEB
2 PVRSIN----CTLRDSGQKSLVMSGPYE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PMRSISENSLVAMDFSGQKSRVIENPTE 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PVRSLN----CTLRDSGQKSLVMSGPYE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 19911230
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90103565
FILING DATE: 09-MAY-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 52, Application US/08459568 Patent No. 5811304 GENERAL INFORMATION:
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1; Gaps
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                                                                                                                                                                                                                                                 DB 2; Length 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 52, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: 2.inc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRE
                                                                                                                                                                                                                                                                                                                   2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-AUG-1995
CLASSFFICATION: 514
                                                                                                                                                                                                                                     Query Match
19.1%; Score 40.5; D
Best Local Similarity 47.4%; Pred. No. 44;
Matches 9; Conservative 7; Mismatches
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APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-WAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
CMBUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6323335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-1 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                        22 TVNKGSLVALGFSDGQEAR 40
                                                                                                                                                                                                                                                                                                                                                                                 4 SISENSLVAMDFS-GOKSR 21
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                                      SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-399-411-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: .66 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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California
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Matches 9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: US
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-516-859A-52
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US-08-516-859A-52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Owery Match
19.1%; Score 40.5; DB 2; Length 66; Best Local Similarity 47.4%; Pred. No. 44;
Matches 9; Conservative 7; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NE-2011 14.

NS-08-399-411-52

Sequence 52, Application US/08399411

Fatent No. 58131008

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 93

CORRESPONDENCES: 93

CORRESPONDENCES: 33

ADDRESSE: Campbell and Flores

STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                           ZIP: 9122
ZIP: 9122
MEDIUM TYPE: Floppy disk
COMPUTER: ENDRY Compatible
COMPUTER: TBM PC COMPATION
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
TILING DATE: 02-10N 1995
CLASSIETCATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTONEY AGENT INFORMATION:
REGISTRATION NUMBER: 31,815
REFERENDE/COCKET NUMBER: P-LJ 1264
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8001
TELEPHONE: (619) 52: SEQUENCE CHARACTERISTICS:
LENGTH: 66 mainto acide
TYPE: aminto acide
TYPE: Innear
                           4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/399;411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Caltryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECHMUNICATION INFORMATION:
TELECHMUNICATION S35-9001
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INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 SISENSLVAMDFS-GQKSR 21
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MEDIUM TYPE: Floppy
STREET: 43/CCITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Cali
COUNTRY: US.
ZIP: 92122
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OPERATING SYSTEM:
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                                              APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 106
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0S-09-528-706-52
5 Sequence 52, Application US/09528706
5 Patent No. 6468985
6 GENERAL INFORMATION:
7 TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: 2inc Finger Proteins
7 TITLE OF SEQUENCES: 106
7 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Campbell & Flores LLP
8 STREET: 437...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 66;
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: LAUPEY LAUFE COMPATIBLE COMPUTER: IBM PC COMPATIBLE SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, Version #1.25 APPLICATION NUMBER: US/09/586,472 FILING DATE: 01-Jun-2000 CLASSIFICATION: <a href="https://documents.com/linearing/linearing/linearing/">UN-2000 CLASSIFICATION: <a href="https://documents.com/linearing/">UN-2000 CLASSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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PRIOR APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-MG-1995
FILING DATE: 18-MG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; Score 40.5; D 47.4%; Pred. No. 44; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-586-472-52
                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION.
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 TVNKGSLVALGFSDGQEAR 40
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Best Local Similarity 47.4%
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 79;
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.4%; Pred. No. +ive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.1%; Score 40.5; 1 47.4%; Pred. No. 57;
                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,706
                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                               P-LJ 1776
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Patent No. 6222029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D. APPLICANT: Duelert, Aymeric
                                                                                                                                                                            NAME: Canpbell, Cathryn A.
REGISTRATION NUMBER: 31.815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 aning acids
                                                                                                                                                                                                                                                                                                                                                                                                                                22 TVNKGSLVALGFSDGQEAR 40
                                                                                                                                                                                                                                                                                                                                                                                                               4 SISENSLVAMDFS-GQKSR 21
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Best Local Similarity 47.4.
For 9, Conservative
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US-09-006-428A-14
                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
US-09-528-706-52
                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 9; Conserve
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US-08-905-223-420
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LENGTH: 79
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FILING DATE: 1997-07-08

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RESULT 18
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APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
TITLE REFERENCE: PZ010P1
CURRENT APPLICATION NUMBER: US/09/227, 357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1999-07-07
                                                                                          ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DENTIFICATION METHOD: VON Heijne matrix;
OTHER INFORMATION: SCORE 4.5
OTHER INFORMATION: SEQ ENSLIILLGGLQG/RV US-08-905-223-420
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EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
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EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 611, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-855
INFORMATION FOR SEX ID NO: 420:
SEQUENCE CHRRACTERISTICS:
LENGTH: 86 amino acids
                                                                                                                                                             STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92.101-35.05
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 RSISENSLVAMDFSGQKSRV 22
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10 RTISENSLIIL-LQGLQGRV 28
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TISSUE TYPE: Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 86 amino acids TYPE: AMINO ACID TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 19.1
Best Local Similarity 50.0
Matches 10; Conservative
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LOCATION: -26..-1
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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US-09-227-357-611
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Gaps
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                                             ER APPLICATION NUMBER: 60/051,931
ER APPLICATION NUMBER: 60/051,931
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
ER FILING DATE: 1997-07-08
ER PELLING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,930
ER FILING DATE: 1997-07-08
ER APPLICATION NUMBER: 60/051,918
ER FILING DATE: 1997-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
BARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER APPLICATION NUMBER: 60/051,928
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EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 611
ENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-08-18
APPLICATION UMBER: 60/056,360
FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
EARLIER FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,950
FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/055,964
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APPLICATION NUMBER: 60/052,732 (ILING DATE: 1997-07-08
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REILING DATE: 1997-07
APPLICATION NUMBER: 60/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1997-08-18
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EARLIER FILING DATE: 1997-06
EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1997-06
EARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 ISENSLVAMDFSGQKSR 21
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US-09-227-357-611
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; ORGANISM: Murine sp. US-09-331-930A-21
                                        -09-331-930A-20
                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: HOMC
US-09-331-930A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-331-930A-21
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                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism: Amino acid CTHER INFORMATION: sequence for beacon from unknown organism US-09-331-930A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
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OTHER INFORMATION: sequence for beacon from unknown organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 18.6%; Score 39.5; DB 4; Length 73; Best Local Similarity 28.9%; Pred. No. 73; Matches 11; Conservative 6; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.6%; Score 39.5; DB 4; Length 73; 28.9%; Pred. No. 73; tive 6; Mismatches 16; Indels
                                                        GENERAL INFOURTHIED TO THEREFOR TILE OF LINEST. PAUL Z.

APPLICANT: ZIMMET, PAUL Z.

APPLICANT: ZIMMET, PAUL Z.

APPLICANT: COLLIER, GREGORY

FILLE OF INVENTANCE: 22975-20007, 00

CURRENT APPLICATION NUMBER: US/09/331, 930A

PRIOR PPLICATION NUMBER: PCT/4U98/00902

PRIOR FILING DATE: 1998-10-30

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-10-31

PRIOR FILING DATE: 1997-11-11

SOFTWARE OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver: Z.1

LENGTH: 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LVAMDFSGQKSRVIENPTEALS----VAVEEGLAWRK 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 LVAMDFSGQKSRVIENPTEALS----VAVEEGLAWRK 42
                   Sequence 2, Application US/09331930A
Patent No. 6436670
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 19, Application US/09331930A
Patent No. 6436670
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 28.9%
Matches 11; Conservative
US-09-331-930A-2
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US-09-331-930A-19
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5; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%; Score 39.5; DB 4; Length 73; 28.9%; Pred. No. 73; Live 6; Mismatches 16; Indels
                                     GENERAL INFORMATION.
APPLICANT: TAIMET, PAUL Z.
APPLICANT: CLILIER, GREGORY
TITLE OF INFORTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: PCT/AU96/00902
PRIOR PAPLICATION NUMBER: PCT/AU96/00902
PRIOR PAPLICATION NUMBER: AU PP0117/97
PRIOR PLING DATE: 1997-10-31
PRIOR APPLICATION NUMBER: AU PP01323/97
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE PATENT ON VERSE SEQ ID NOS: 27
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/09331930A
Patent No. 643670
GENERAL INFORMATION:
APPLICANT: ZIMMET, PAUL Z.
APPLICANT: ZOLLIER, GERGENE
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
CURRENT FLING DATE: 1999-06-30
CURRENT FLING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: PCT/AU98/00902
PRIOR FILING DATE: 1999-10-31
PRIOR FILING DATE: 1999-10-31
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTING VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LVAMDFSGQKSRVIENPTEALS----VAVEEGLAWRK 42
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Sequence 20, Application US/09331930A
Patent No. 6436670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 22
US-09-331-930A-24
; Sequence 24, Application US/09331930A
; Patent No. 6436670
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 28.9%
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 18.69
Best Local Similarity 28.99
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Homo sapiens
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TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
ADDRESSES: WOLF, GREENFIELD & SACKS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/09081320
Patent No. 6093544
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gensalves, Dennis
APPLICANT: Meng, Baozhong
TITLE OF INVENTION: RUPESTRIS STEM PITTING ASSOCIATED VIRUS
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON, Hargrave, Devans & Doyle LLP
STREET: Clinco Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.4%; Score 39; DB 3; Length 68; 30.4%; Pred. No. 79; tive 9; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARIE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION
CLASSIFICATION
PRIOR APPLICATION NATA:
PRIOR APPLICATION NUMBER: US 08/596,291
FILING DATE:
O9-AUG-1996
APPLICATION NUMBER: US 08/115,573
FILING DATE:
PRIOR APPLICATION NUMBER: DCT/US94/09943
FILING DATE:
O1-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDMARD R.
REGISTATION NUMBER: 1,616
REFERENCE/DOCKET NUMBER: LO461/7003
TELECHONE: 617-720-3500
TELECHONE: 617-720-3500
                                                                                                                                                                                                                                   COMPUTER FEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                             ADDRESSEE: WOLF, GREEN. --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 30.43
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                         MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sin
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: U.S.A.
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US-09-100-804-30
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US-09-081-320-9
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Best Local 3
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Patent No. 6066472
GENERAL INFORMATIONE
APPLICANT: GONES, LEONEL JORGE
APPLICANT: CLAESSON WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
APPLICANT: ZIMMET, PAUL Z.
APPLICANT: COLLIER, GREGORY
TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT APPLICATION WUMBER: US/09/331,930A
CURRENT APPLICATION WUMBER: PCT/AU98/00902
PRIOR APPLICATION WUMBER: PCT/AU98/00902
PRIOR APPLICATION WUMBER: AU PP0117/97
PRIOR APPLICATION WUMBER: AU PP013/97
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ZIMMET, PAUL Z.
APPLICANT: ZIMMET, PAUL Z.
APPLICANT: COLLIER, GREGORY
FILTE OF INVENTION: A NOVEL GENE AND USES THEREFOR
FILE REFERENCE: 22975-20007.00
CURRENT APPLICATION NUMBER: DS/99/331,930A
CURRENT FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-10-30
PRIOR FILING DATE: 1997-10-31
PRIOR FILING DATE: 1997-11-11
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN OFF: 23
SSETARRE: PATENTIN OFF: 2.1
SEQ ID NOS: 27
LENGTH: 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 VVCNDRLGKKVRVKCNTDDTIGDLKKLIAAQTGTRWNK 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.6%; Score 39.5; Di
Best Local Similarity 28.9%; Pred. No. 73;
Matches 11; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25, Application US/09331930A Patent No. 6436670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-331-930A-25
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Oryza sativa
US-09-331-930A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-331-930A-25
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Gaps 4;

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2; Gaps
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18.4%; Score 39; DB 3; Length 80;
Best Local Similarity 46.2%; Pred. No. 98;
Matches 12; Conservative 5; Mismatches 7; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATUG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,320
CLASSIFCATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/069,902
FILING DATE: JO-MAY-1997
APPLICATION NUMBER: US 60/069,902
FILING DATE: JT-DEC-1997
APPLICATION NUMBER: 30,727
ATORNEY/AGENT INFORMATION:
NAME: GOldman, Michael L.
REGISTRATION NUMBER: 30,727
TELEFONMUNICATION NUMBER: 30,727
TELEFONMUNICATION NUMBER: 19603/1722
TELEFONMUNICATION NUMBER: 19603/1722
TELEFONMUNICATION OF SEG-100
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acid
STRANDENSS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-081-320-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 KSRVIEN--PTEALSVAVEEGLAWRK 42
| | | | | | | | | | |
| 6 ESILIENCGPSEALASTVKEVLGGLK 65
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Search completed: March 28, 2003, 09:09:31 Job time : 30.5276 secs

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on:

March 28, 2003, 08:55:25; Search time 33.8583 Seconds (without alignments)
169.228 Million cell updates/sec

1 PWRSISENSLVAMDFSGQKS......ENPTEALSVAVEEGLAWRKK 43 Sequence:

908470 seqs, 133250620 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 40 Maximum DB seq length: 90

Post-processing: Minimum Match 1008

Maximum Match 1008

Listing first 1000 summaries

Listing first 1000 summaries

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4 /SIDS2/gcdata/geneseq/geneseqp-embl/AA1981.DAT:

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7 /SIDS2/gcdata/geneseq/geneseqp-embl/AA1981.DAT:

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13 /SIDS2/gcdata/geneseq/geneseqp-embl/AA1991.DAT:

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24 /SIDS2/gcdata/geneseq/geneseqp-embl/AA1991.DAT:

25 /SIDS2/gcdata/geneseq/geneseqp-embl/AA1991.DAT:

27 /SIDS2/gcdata

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Dentide derived fr	Dentide derived in	Pentide derived in	Dentide derived fr	Dentide derived II	Dentide derived in	Dontide delived in	Pertide derived fr			
		ID	AAB18941	AAB18942	AAB18937	AAB18938	AAB18949	AAB18950	AAB18957	AAB18958	AAB18945	AAB18946	
		DB	21	21	7	21	21	21	21	77	21	21	
		ength	43	84	43	84	43	82	43	80	43	85	
оp	Query	e Match Length DB I	100.0	100.0	96.7	96.7	79.7	79.7	76.4	76.4	75.9	75.9	
		Score	212	212	205	205	169	169	162	162	161	161	
	Result	NO.		7	٣	4	2	9	7	80	6	10	

Peptide derived fr Human ORFX protein Human OPFIde enco Human Secreted pro Novel central nerv Novel central nerv Propionibacterium		Human polypeptide Human reproductive Propionibacterium Human nervous syst Propionibacterium Bropionibacterium Bropioniba	H. Pylori GHPO 138 Propionibacterium Novel human digestive sy Arabidopsis thalia Human bone marrow Peptide #7275 enco Peptide #7275 enco Human peptide enco P. obesus beacon p Israeli sand rat b Human polypeptide Human nolypeptide Human ilver associ Human liver associ Human liver associ Human liver associ Human liver alge Novel human diagno Arabidopsis thalia Enterococcus faeca
21 AAB189 21 AAB189 22 AAB189 23 AAB189 22 AAG761 23 ABP023 23 ABP023 22 AAG72 21 AAG72 22 AAU871 22 AAU874	22 AAM65249 22 AAM84732 20 AAM8732 22 AAM87732 22 AAM87732 22 AAM87783 22 AAM87783 22 AAM87783 22 AAM878284 22 AAM66679 22 AAM66679 22 AAM6679 22 AAM65679 22 AAM65679 22 AAM65679 22 AAM85610 22 AAM85610 22 AAM85610 22 AAM85610 23 AAM85610 23 AAM85610 23 AAM85610	22 AAM1466 22 AAM56493 22 ABG6590 22 ABG6786 22 ABG0735 22 AAB09814 21 AAG19914 21 AAG5105 21 AAG5105 22 ABB42761 22 ABB42761 22 ABB42761 22 ABM6565 22 AAM6565 23 ABG6572 23 ABG6572 20 AAM6572 20 AAM6572 20 AAM6572	19 AAW98525 22 AAU45158 22 AAU52574 22 AAW52537 21 AAG54855 21 AAG641701 23 AAW33013 23 AAW33013 23 AAW39680 22 AAW39680
75.0 75.0 75.0 75.0 75.0 75.0 75.0 75.0	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	11.5 5 11.5 5 11.5 5 14.1 11.1 11.1 11.1 11.1 11.1 11.1 11.1	40 18.9 70 40 18.9 71 40 18.9 71 40 18.9 71 40 18.9 71 40 18.9 71 40 18.9 72 40 18.9 72 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5
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662 662 663 663 663 663 663 663 663 663	51 51 51 51 65 67 71	4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	4 4 4 4 10 10 10 10 10 10 10 10 10 10 10 10 10	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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38 38 38 38 38 38 37 5	23 24 24 24 24 24 24 24 24 24 24 24 24 24			
	·			2008 2008 2008 2008 2008 2008 2008 2008
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ALIGNMENTS

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Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
AAB18941 standard; peptide; 43 AA.
                                                                     (first entry)
                                                                 08-FEB-2001
                                 AAB18941;
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Phosphorylated insulin receptor interacting region; Grb7 family protein insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.

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Homo saptens.
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        21-SEP-2000
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14-MAR-2000; 2000WO-FR00613.

99FR-0003159. 15-MAR-1999;

(CNRS) CNRS CENT NAT RECH SCI.

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Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases that are potentially useful for treating insulin-associated diseases and syndrome X.
                                              Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity
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                                                                                                              Claim 2; Page 25; 46pp; French.
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SIGN which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine Kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, and syndrome X.
stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome and syndrome X.
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iive 0; Mismatches (
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetés and obesity but also polycystic ovarian syndrome
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96.7%; Score 205; DB 21; Length 43; 93.0%; Pred. No. 9.3e-24; Live 3; Mismatches 0; Indels

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Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.
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                                                                                                   Homo sapiens.
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR: SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents particularly dispetes and obesity but also polycystic ovarian syndrome and syndrome X.
                                                                    Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity
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Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;
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                                                                                                                                               Claim 2; Page 30; 46pp; French.
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PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the limslin receptor can stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome
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Pred. No. 3.3e-17;
4; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                   1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 34-35; 46pp; French.
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74.48;
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Score 162; DB 21; Length 80; Pred. No. 7.9e-17;

76.48;

74.48;

Query Match Best Local Similarity

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7; Indels
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                                                          1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 43
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   4; Mismatches
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78.0%;
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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR:5H2 (src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times affect in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases that are potentially useful for treating insulin-associated diseases, and syndrome X.
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Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
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                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587566/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 AA;
                                                                                                                                                     WO200055634-A1.
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                                                                                                                                                                                                                                                                   15-MAR-1999;
                                                                                                                                                                                        21-SEP-2000.
                                                                                                                Mus muris.
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Seguence Query Match

Matches

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AAB18953;

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0; Gaps

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Gaps

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B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SH2 (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times greater in presence of SH2 (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine Kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, particularly diabetes and obesity but also polycystic ovarian syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B18937-64 represent the PIR (phosphorylated insulin receptor interacting region) or PIR-SIZ (Src homology 2) domains of a Grb7 family protein. PIR is the actual binding region but its effect is about 10 times preater in presence of SIZ (which by itself is inactive). Agents that affect binding between the peptides and the insulin receptor can stimulate or inhibit tyrosine kinase activity of the receptor. The peptides are used for screening molecules for ability to treat diseases in which insulin is implicated. The peptides are used to identify agents that are potentially useful for treating insulin-associated diseases, and syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragments of Grb family proteins to identify compounds are useful in
treating insulin-associated diseases, particularly diabetes and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylated insulin receptor interacting region; Grb7 family protein insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome; syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bereziat V, Girard J;
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
                                                                                                                                                                                                                                                                              Score 159; DB 21; Length 43;
Pred. No. 9.6e-17;
6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                         1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                                                            Burnol A, Perdereau D, Kasus-Jacobi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB18954 standard; peptide; 80 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 32; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAR-2000; 2000WO-FR00613.
                                                                                                                                                                                                                                                                              75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99FR-0003159.
                                                                                                                                                                                                                                                                                               69.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-587566/55.
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                             43 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB18954;
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80 AA;

Sequence

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                                                                                                                                                                                                                                                                                               Phosphorylated insulin receptor interacting region; Grb7 family protein; insulin receptor; tyrosine kinase; insulin; insulin-associated disease; diabetes; obesity; polycystic ovarian syndrome, syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragments of Grb family proteins to identify compounds are useful in treating insulin-associated diseases, particularly diabetes and obesity
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Burnol A, Perdereau D, Kasus-Jacobi A, Bereziat V, Girard J;
                              ;
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                                                                                                                                                                                                                                                                   Peptide derived from the PIR or PIR-SH2 domain of Grb7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 80;
 Length 80;
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                              7; Indels
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                                                               43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PLRSVSDNTLVAMDFSGHAGRVIDNPREALSAAMEEAQAWRKK 55
                                                                                 13 PLRSVSDNTLVAMDFSGHAGRVIDNPREALSAAMEEAQAWRKK 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.0%; Score 159; DB 21;
69.8%; Pred. No. 2.3e-16;
tive 6; Mismatches 7;
                                                               1 PMRSISENSLVAMDFSGQKSRVIENPTEALSVAVEEGLAWRKK
Score 159; DB 21;
Pred. No. 2.3e-16;
6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP08708 standard; Protein; 67 AA.
                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 37; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                         AAB18962 standard; peptide; 80
 75.0%;
69.8%;
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                                                                                                                                                                                                                                       08-FEB-2001 (first entry)
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                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-587566/55
                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 AA;
                                                                                                                                                                                                                                                                                                                                                                                                WO200055634-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and syndrome X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30;
                                                                                                                                                                                                                                                                                                                                                                   Mus muris.
                                                                                                                                                                                                        AAB18962;
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   Query Match
Best Local S
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                                  Matches
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                                                                                                                                          RESULT 14
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ID ABPC
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17 LGFSFSGPKSRVLSTSLHCPMPVEVLAEKEHGGFQW 52.

AAU30892 standard; Protein; 72 AA.

RESULT 16 AAU30892

Human; vaccination; gene therapy; nutritional supplement; stem cell proliferation; haematopoiesis; nerve tissue regeneration; immune suppression; immune stimulation; anti-inflammatory; leukaemia.

16-APR-2001; 2001WO-US08656. 18-APR-2000; 2000US-0552929. 26-JAN-2001; 2001US-0770160.

WO200179449-A2.

25-OCT-2001,

Homo sapiens.

Novel human secreted protein #1383.

(first entry)

18-DEC-2001

AAU30892;

us-09-936-697-5.max.rag

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder: psoriasis; benign tumour; haemorrhage; cardiovascular disease, diabetes mellitus; neurodegenerative disorder; hypertension; hypothyroidism; cholesterol ester storage disease; limmune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.1%; Score 49; DB 23; Length 67; 33.3%; Pred. No. 11; tive 3; Mismatches 15; Indels
                                     Human ORFX protein sequence SEQ ID NO:17398.
                                                                                                                                                                                                       29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                         30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                  24-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                           Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                        (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                             WPI; 2002-106308/14.
N-PSDB; ABN24460.
                                                                                                                                                                WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AA;
                                                                                                                                               Homo sapiens.
                                                                                                                                                                                     06-DEC-2001.
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The present invention describes substantially purified human proteins

C (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1)

to the specification). ABM15/62 to ABM27552 encode the human ORFX

in the specification). ABM15/62 to ABM27552 encode the human ORFX

c retains given in ABP00101 to ABM127552 encode the human ORFX

c retains given in ABP00101 to ABM15/65 encode the human ORFX

c retains given in ABP00101 to ABM15/65 encode the human ORFX

c specimens or preventing a pathology associated with an ORFX-associated

c specimen or preventing a pathology associated with an ORFX-associated

c syndrome associated with ORFX-associated disorder. ORFX polynucleotide

c streatment of cancer, hyperproliferative disorders, cirrhosis of liver,

c psoriasis, benign tumours, keloid, degenerative disorders; haemorrhage,

c transplantation, cardiovascular disoases, disorders related to organ

c transplantation, cardiovascular diseases, disorders, infectious

c transplantation, cardiovascular diseases, disorders, infectious

c transplantation, avarious immune deficiencies and disorders, infectious

carthritis, autoimmune disorders such as multiple sclerosis, theumatoid

disease and autoimmune infimamatory eye disease. ORFX proteins are also

c bone degenerative disorders, or periodontal disease, and for gut

renerfusion intimative in various intensions and constitute for the constitution and treatment of lung or liver fiberosis,

c renerfusion intimation and treatment of lung or liver fiberosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reperfusion injury in various tissues and conditions resulting from systemic cytokine damage.
Disclosure; SEQ ID 17398; 1037pp; English.
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11 VAMDFSGQKSRVIEN-----PTEALSVAVEEGLAW 40

Local Similarity 33.39 nes 12; Conservative

Best Loca Matches

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The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents also useful for identifying a part and antagonists) that bind to them. Cells of or use in treatment of a pathology related to aberran expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptide. Vectors comprising the nucleic acids encoding the polypeptide and earls genetically comprised to express them are also useful for producing the proteins are useful in genetic vaccination, testing and cincrase stem cell proliferation; to regulate haematopoiesis: and in increase stem cell proliferation; to regulate haematopoiesis; and in the timmune suppression and/or atimulation; as anti-inflammatory agents; and conclusion in treatment of leukaemias. AAU79510-AAU33304 represent the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 4%; DB 22; Length 72;
26.8%; Pred. No. 17;
Live 13; Mismatches 14; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 PMRSISENSLVAMDFSGQKSRV----IENPTEALSVA----VEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 366; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG76197 standard; Protein; 73 AA.
                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 26.8%
les 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611725/70.
                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 AA;
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ANH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene the colon cancer antigens have cytostatic activity and can be used in gene the colon cancer antigens have cytostatic activity and can be used in gene prevention, color cangers and treatment of diseases associated with happropriate P compared and treatment of diseases associated with nappropriate P color cancer associated with decreased expression rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing including anticular proteins or to supplement the patients own production of P. Color cancer associated Ps. Color cance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                     cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 TISENLFATTGYPGKMASQFQIHHLGHPQPILMGSVAVGSGLSWHR 56
                                                                                 Human colon cancer antigen protein SEQ ID NO:6961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX protein sequence SEQ ID NO:4630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 8390; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ruben SM, Barash SC, Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC.
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                                 03-SEP-2001 (first entry)
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Best Local Similarity 30.4
Matches 14; Conservative
                                                                                                                                        Human; colon cancer; colorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-235357/24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAH35602
                                                                                                                                                                                                                                                                    WO200122920-A2.
                                                                                                                                                                                                                    Homo sapiens.
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                        05-APR-2001.
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORRY, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN27252 encode the human ORRX proteins are useful for proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORRY-associated disorder. ORFX polynucleotide syndrome associated with Rora-associated disorder. ORFX polynucleotide syndrome associated with Rora-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the creatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, in the carecarthritis, meurodegenerative disorders, disorders, infectious storage disease, various immune deficiencies and disorders, infectious diseases, autolimmune disorders such as multiple sclerosis, rheumatoid arthritis, autolimmune thyroiditis, myssthenia gravis, graft-versus-host consequential pourns, incisions, ulcers, for treating osteoporosis, consequential diseases, and for gut consequential diseases. An one degenerative disorders, or periodontal disease, and for gut consequential diseases, and for gut consequential diseases, and for gut consequential diseases, and for gut consequential disease, and disorders in perfusion or regeneration and treatment of lung or liver fibrosis, consequential diseases.
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO and fite.int/pub/published_pct_sequences.
                degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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2
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36.4%; Pred. No. 29;
Live 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 WSGO---VLENAVRWGLRREPLNVSLQNGKSWR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID 4630; 1037pp; English.
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ID ABG47266 standard; Peptide; 84 AA.
XX
                                                                                                                                                                                                                                                                                                                             29-MAY-2001; 2001WO-US10836.
                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 36.49 nes 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-106308/14.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABN18076.
                                                                                                                                                                                                                                  WO200192523-A2.
                                                                                                                                                                                          Homo sapiens.
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ABG47266:

us-09-936-697-5.max.rag

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Human peptide encoded by genome-derived single exon probe SEQ ID 36931.
                                                                                                                                          Human; single exon probe; asthma; lung cancer; COPD; ILD; fahronic obstructive pulmonary disease; interstitial lung disease; therstitial lung disease; tuberous sclerosis; contents sclerosis; disease; Niemann-Plok disease; pulmonary histicoytosis; lymphangioleicompann-Plok disease; pulmonary histicoytosis; lymphangioleicompannosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary sivenesis; pulmonary displasis; hypertension; hypertension;
19-AUG-2002 (first entry)
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WO200186003-A2. Homo sapiens. 15-NOV-2001. 30-JAN-2001; 2001WO-US00665. 04-FEB-2000; 2000US-180312P. 30-JUN-2000; 26-MAY-2000;

2000US-207456P. 2000US-0608408. 03-AUG-2000; 2000US-0632366. 21-SEP-2000; 2000US-234687P. 27-SEP-2000; 2000US-236359P. 04-OCT-2000; 2000GB-0024263. Hanzel DK, Chen W, Rank DR;

WPI; 2002-114183/15.

Spatially-addressable set of single exon nucleic acid probes, used to measure gene expression in human lung samples -Claim 27; SEQ ID No 36931; 634pp; English.

The Invention relates to a spatially-addressable set of single exon cucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising the acid probes having one of probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at thigh stringency to a collection of detectably labeled mucleic acid expression in a collection of detectably labeled nucleic acids derived from human lung, comprising of a collection of detectably labeled nucleic acids derived from human lung, comprising of a collection of detectably labeled nucleic acids derived from human lung comprising of a collection of detectably labeled nucleic acids derived from human lung comprising of a collection of detectably labeled nucleic acids derived from human lung collection of detectably bound to each probe of the array; identifying exons in a eukaryotic acids derived from human lung collection at least one exon from genomic sequences of the eukaryote; and (b) detecting at least one exon from genomic sequences and algorithmically predicting at least one exon from genomic sequences contributed above mentioned microarray; assigning exons to a single exon probe, in the above mentioned microarray; assigning exons in a single exon in several expression of the exons in the tissues and/or cell types using phybridisation to a single exon in expression of the exons in the tissues and/or cell types using phybridisation to a single exon for the exons in the tissues and/or cell types using phybridisation or encoded by the exons and an analysis and for the probes are used for gene correct probes/open reading frames (ORF). The probes are used for gene where such as asthma, lung derived mank and for the study of lung derived mank and for the study of lung are seen common particularly such as asthma, lung derived mank and for the study of lung parent characterizing the services and particularly sequences.

72 AA;

Seguence

3 Niemann-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary pulmonary alveolar proteinosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic and hyaline membrane disease. The present sequence is a peptide/protein Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic fip. who.int/pub/published_pct_sequences. Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping. Gaps The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly, to the 3' iron oilso-dr primed CDNA libraries. Such ESTs are not well sulted for those cases where longer cDNA sequences have been obtained isolating cDNA sequences have been obtained, the full 5' ends of mRNAs and even in Those cases where longer CDNA sequences have been obtained, the full 5' ends and can therefore be used to obtain full length cDNAs with intext 5' DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and requilatory sequences. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors. New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures 7; Indels 26; 17 GOKSRVIENP------EEGLAWRKK 43 11 GOKARLLSRPLRGVSGKHCLTFFYHMYGGGTGLLSVYLKKEEDSEESLLWRRR 63 21.2%; Score 45; DB 23; Length 84; 26.4%; Pred. No. 59; Live 6; Mismatches 7; Indels Dumas Milne Edwards J, Duclert A, Giordano J; Claim 13; SEQ ID 7421; 71pp + CD-ROM; English. Human secreted protein, SEQ ID NO: 7421. AAG03340 standard; Protein; 72 AA. 21-FEB-2000; 2000EP-0200610. 26-FEB-1999; 99US-0122487. 06-OCT-2000 (first entry) Local Similarity 26.4 WPI; 2000-500381/45. 84 AA; N-PSDB; AAC03346 5' EST; (GEST) GENSET. Homo sapiens. EP1033401-A2. 06-SEP-2000. Sequence Query Match AAG03340; Matches RESULT 20 δ us-09-936-697-5.max.rag

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2000US-0241787.
2000US-0241808.
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2000US-0246528
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13-0CT-2000)
13-0CT-2000)
20-0CT-2000)
20-0C
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02-OCT-2000;
02-OCT-2000;
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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; phyperpoliferative disorder; neoplasm; cardiovascular disorder; carebrovascular disorder; ischaemla; anglogenesis; nervous system disorder; Alzheimer's disease; AIDS; ocular disorder; acquired immunodeficiency vitus; dysphagia; gastrointestinal disorder; adenocarcinoma; reproductive system disorder; testicular feminisation; endocrine disorder; diabetes; cancer; leukaemia; neovascularisation; arspiratory disorder; renal disorder; kidney failure; blood disorder; food additive; food preservative; gene therapy.
                                               Gaps
              y Match 21.0%; Score 44.5; DB 21; Length 72; Local Similarity 50.0%; Pred. No. 57; hes 10; Conservative 4; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                       Novel central nervous system protein #74.
                                                                                                                                                                                        AAU87164 standard; Protein; 74 AA
                                                                                 21 RVIENPTEALSVAVEEGLAW 40
                                                                                                   18 - APR-2000; 2000US-0198123
19 - MAY - 2000; 2000US-0205515.
07 - UUN-2000; 2000US-0209467.
28 - JUN-2000; 2000US-0214886.
30 - JUN-2000; 2000US-0214886.
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2000US-0227182
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                                                                                                                                                                                                                                                          05-JUN-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                                                                                                             AAU87164;
                   Query Match
                                                                                                                                                           RESULT 21
AAU87164
                                    Best Loc
Matches
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Central nervous system; CNS; autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; neoplasm; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; AlDS; ocular disorder; acquired immunodeficiency virus; dysphagia; gastrointestinal disorder; endocrine disorder; diabetes; cancer; leukaemis; neovascularisation; respiratory disorder; renal disorder; leukaemis; neovascularisation; myocardial infaction; wound healing; cell proliferation; skin aging; food additive; food preservative; gene therapy.
                                                        20 SITENGLIPKDYRSLKTQYLQSYGPEHLLTFSNLRXAGLLTXQAPGDNXTAWRVK 74
                                                                                                                                                                                                                                                                   Novel central nervous system protein #390.
                                                                                                                                                   AAU87480 standard; Protein; 74 AA
                                                                                                                                                                                                                           05-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-2001; 2001WO-US01332.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200155318-A2.
                                                                                                                                                                                             AAU87480;
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05-SEP-2000;
                                                                                                                RESULT 22
AAU87480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes an isolated nucleic acid molecule (I) encoding a covel central nervous system protein (I) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a dutoimmune diseases e.g. rheumatoid arthritis, hypertholiferative cc disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. or cardiovascular disorders any lotrophic lateral sclerosis, informatic e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. orneal infection, gastrointestinal disorders e.g. dysphagia, cc. e.g. corneal infections caused by bacteria, viruses cc. e.g. orneal infections gastrointestinal disorders e.g. dysphagia, call and pituliary dwarfism, cancers and disorders e.g. dysphagia, and pituliary dwarfism, cancers and disorders e.g. diabetes cc. and pituliary dwarfism, cancers and disorders e.g. malignancies, or lespiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. influence of ceptibelial cell proliferation, to prevent skin aging due to sumburn, to primary tissues, to regenerate tissues and in chemotaxis. The primary tissues can also be used to aid wound healing and primary tissues, to regenerate tissues and in chemotaxis. The increase or decrease storage capabilities, fat content, libid, protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16; Indels 15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 22; Length 74;
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23.6%; Pred. No. 59,
've 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; SEQ ID No 682; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                     17-NOV-2000; 2000US-0249265
17-NOV-2000; 2000US-0249295
17-NOV-2000; 2000US-0249299
17-NOV-2000; 2000US-0249299
01-DEC-2000; 2000US-025099
05-DEC-2000; 2000US-025099
05-DEC-2000; 2000US-0251030
05-DEC-2000; 2000US-0251080
06-DEC-2000; 2000US-0251186
08-DEC-2000; 2000US-02511869
08-DEC-2000; 2000US-02511869
08-DEC-2000; 2000US-02511869
08-DEC-2000; 2000US-02511869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 23.67
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-581633/65.
N-PSDB; ABK43494.
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06-SEP-2000; 2000US-0220437.
06-SEP-2000; 2000US-0220437.
08-SEP-2000; 2000US-0220433.
08-SEP-2000; 2000US-0221443.
08-SEP-2000; 2000US-0221443.
08-SEP-2000; 2000US-0221443.
08-SEP-2000; 2000US-0221443.
08-SEP-2000; 2000US-0231281.
14-SEP-2000; 2000US-0231281.
15-SEP-2000; 200
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2000US-0249215.
2000US-0249216.
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The invention describes an isolated nucleic acid molecule (1) encoding a novel central nervous system protein. (1) and polypeptides (III) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. But are diagnosed or treated include the diagnosed or treated include attoinment diseases e.g. rheumatoid arthritis, hyperproliferative cardiomases e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. Alzhehmer's disease and anylotrophic lateral sclerosis, infections caused by bacteria, viruses c.g. Acquired immunodeficiency virus (AIDS) and fund, coular disorders e.g. denocarcinomas and irritable bowel syndrome, reproductive system of principal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system of pituitary dwarfism, cancers and disorders e.g. diabetes and pituitary dwarfism, cancers and disorders e.g. malignancies, claukeamia, disorders involving neovascularisation e.g. malignancies, crespiratory disorders involving neovascularisation e.g. mycoarders e.g. cute kidney failure and blood related disorders e.g. mycoarders e.g. cute kidney failure and blood related disorders e.g. mycoarders e.g. mycoardial cell proliferation, to prevent skin aging due to sumbrun, to primary tissues, to regenerate tissues and in chemicaxis. The primary tissues, to regenerate tissues and in chemicaxis. The primary tissues or decrease storage capabilities, fat content, lipid, protein,
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Best Local Similarity 23.6%; Pred. No. 59;
Matches 13; Conservative 11; Mismatches 16; Indels 15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid encoding a protein for diagnosing, preventing, treating or ameliorating medical conditions and food additives or preservatives -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 9; SEQ ID No 998; 837pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
AAU41349
ID AAU41349 standard; Protein; 79 AA.
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
17-NOV-2000; 2000US-0249217.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249267.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-025198.
05-DEC-2000; 2000US-025198.
05-DEC-2000; 2000US-0251866.
06-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
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N-PSDB; ABK43810.
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic to the treatment, prevention and their associated DNA sequences are used in the treatment, prevention and dagnosis of medical conditions caused in pustulosis, hypertosis and osteomyclitis) weelts and endophthalmitis.

CC acnes is also involved in infections of bone, joints and endophthalmitis. nervous system, however it is particularly involved in the inflammatory presence or absence of p. acnes in a patient comprises contacting to sample with a binding agent that binds to the protein of an entrail cc and determining the amount of bound protein in the sample. The polypeptides may be used as antiquent in the sample. The downregulate expression and activity of P. acnes production of antibodies can be used to downregulate expression and activity of P. acnes production of antibodies can be used to downregulate expression and activity of P. acnes productions of antibodies and catagents for determining P. acnes infections. The antibodies can be used as naminal activity of P. acnes production as any also be used as consigning the across infections. The antibodies can be used as consigned immunosorbent assay (ELISA).

CC and determining P. acnes infections. The antibodies can be used as consigning the across that across the production and activity of P. acnes production as any also be used as consigning the across that across presence, for example, by specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                  SAPHO syndrome, synovitis; acne, pustulosis; hypertosis; osteomyelitis; inflammatcry lesion; acne vulgaris; enzyme linked system; Elish, dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes polypeptides and nucleic acids useful for treating against and diagnosing infections, especially useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang SS, Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              For the control of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                        Propionibacterium acnes immunogenic protein #2245.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred No. 65;
10; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitcham JL, Wang Sg
, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 SISENSLVAMDFSGOKSRVIENPTEALSVAVEEGLAWRKK 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 SLVNSBVTALSREGPSNRV---PTRSLACATRHGVCSRER 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; SEQ ID No 2544; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU62249 standard; Protein; 90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2001; 2001WO-US12865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                              13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skeiky YAW, Persing DH, M.
L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-616774/71.
N-PSDB; AAS59515.
                                                                                                                                                                                                                                                                                                                                                                                           WO200181581-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-2001.
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU62249
ID AAU6.
XX
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Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic complete treatment, prevention and diagnosts of medical conditions caused in the treatment, prevention and diagnosts of medical conditions caused by acnes. The disorders include SAHO syndrome (synovitis, acne, practions, hypertosis and osteomyelitis), uveitis and endophthalmits. CC new constraints in infections of bone, Johns and the central presence or absence of p. acnes ungaris. A method for detecting the presence or absence of p. acnes in a patient comprises contacting a polypeptides may be used as antigens in the proteins of the invention of specific for P. acnes proteins. These antibodies can be used to downsqulate expression and activity of P. acnes polypeptides and contacting a polypeptides may be used as antigens in the production of antibodies can be used to downsqulate expression and activity of P. acnes polypeptides and carry in the sequence acts for example, by specification, but was obtained in electronic format directly from WIPO.
                                                                                  SAPHO syndrome, synovitis, acne, pustulosis, hypertosis; osteomyelltis; endophthalmitis; bone, joint, central nervous system; ELISA, inflammatcry lesson, acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7:
                                                                                                                                                                                                                                                                                                                                                                                  Wang SS, Bhatia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                        Propionibacterium acnes immunogenic protein #23145.
                                                                                                                                                                                                                                                                                                                                                                     ing DH, Mitcham JL, Wang S:
Zhang Y, Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID No 23444; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.0%; Score 44.5;
33.3%; Pred. No. 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 SCOKSRVIENP-----TEALSVAVEEGLAWR 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|: | : :|
19 TGEASEEVTHPLVDEGSATNTLLEAVQLGLAWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM94366 standard; Protein; 47 AA.
                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US12865.
                                 (first entry)
                                                                                                                                                                                                                                                                      21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9:
                                                                                                                                                         Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                    Persing DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                            L'maisonneuve J,
                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAS59624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 11; Conserv
                             27-FEB-2002
                                                                                                                                                                                                                 01-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                Skeiky YAW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
RESULT 25
AAM94366
ID AAM94
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Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy.
                                                                                                                                                                                                  Human reproductive system related antigen SEQ ID NO: 3024.
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                                                                                     21-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200155320-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

14-AUG-2000

18-AUG-2000

18-AUG-2000

18-AUG-2000

18-AUG-2000

10-SEP-2000

11-SEP-2000

11-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-2001.
AAM94366;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition -
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; SEQ ID NO 3024; 1297pp + Sequence Listing; English.
                                                                                                                                                                                                                                          Rosen CA, Barash SC, Ruben SM;
08-DEC-2000; 2000US-0251856.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251899.
11-DEC-2000; 2000US-0251990.
05-JAN-2001; 2001US-0254097.
                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                          WPI; 2001-465570/50.
N-PSDB; AAL00336.
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Ouery Match
Best Local Similarity 44.4%; Score 44; DB 22; Length 47;
Matches 8; Conservative 5; Mismatches 5; Indels 7 SRVLKGPTNIVSLSVNSG 24 20 SRVIENPTEALSVAVEEG 37 ò

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0; Gaps

Search completed: March 28, 2003, 09:05:30 Job time : 58.8583 secs